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Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, J. Christopher  
Gurney, Austin L.  
Hillan, Kenneth J  
Kljavin, Ivar J.  
Kuo, Sophia S.  
Napier, Mary A.  
Pan, James;  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Shelton, David L.  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William I.

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Asp Glu Ser Val Gly Ser Lys Thr Arg Arg Ala Phe Leu Tyr Leu  
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Ala Ala Phe Pro Phe Met Asp Ala Met Ala Trp Thr His Ala Gly  
140 145 150  
Ile Leu Leu Lys His Lys Tyr Ser Phe Leu Val Gly Cys Ala Ser  
155 160 165  
Ile Ser Asp Val Ile Ala Gln Val Val Phe Val Ala Ile Leu Leu  
170 175 180  
His Ser His Leu Glu Cys Arg Glu Pro Leu Leu Ile Pro Ile Leu  
185 190 195  
Ser Leu Tyr Met Gly Ala Leu Val Arg Cys Thr Thr Leu Cys Leu  
200 205 210

Gly Tyr Tyr Lys Asn Ile His Asp Ile Ile Pro Asp Arg Ser Gly  
215 220 225

Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe  
230 235 240

Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg  
245 250 255

Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser  
260 265 270

Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val  
275 280 285

Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr  
290 295 300

Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr  
305 310 315

Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val  
320 325 330

Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr  
335 340 345

Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp  
350 355 360

Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser  
365 370 375

Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp  
380 385 390

Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val  
395 400 405

Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr  
410 415 420

Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala  
425 430 435

Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr  
440 445 450

Val Tyr Arg Lys Gln Lys Lys Met Glu Asn Glu Ser Ala Thr  
455 460 465

Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu  
470 475 480

Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu  
485 490

<210> 8  
<211> 535  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 66, 96, 387  
<223> unknown base

<400> 8  
cctgacagaaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50  
tgagcttctg gtgccontttg gctctaattc tggccacaca gagaancagt 100  
cggccttattt tcaaccttctt tggttcccgg gaccttggtg gcagttctgc 150  
agccacagag gcagttggcga ttttgacagc cacataccct gtgggtcaca 200  
tgccatacgg ctgggttgcacg gaaatccgtg ctgtgtatcc tgcttcgac 250  
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
ggcccacatc aagaagttca ctttcgtctg catggctctg tcactcacgc 350  
tctgtttcgt gatgttttg acacccaacg tgtctngaa aatcttgata 400  
gacatcatcg gagtgactt tgccttgca gaactctgtg ttgttcctt 450  
gcggatcttc tccttcttcc cagttccagt cacagtgagg ggcgcacatca 500  
ccgggtggct gatgacactg aagaaaaaccc tcgtc 535

<210> 9  
<211> 434  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,  
293, 296, 305, 336, 358, 361  
<223> unknown base

<400> 9  
tgacggaatc ccgggctggg tatcctggtt tngacaagat aaaccccccag 50  
caanaaaattt gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100  
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtat 150  
gttttggaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200  
tggantttgc ctttgcagaa ntttgnngntg ttcccttgcg gatttctcc 250  
tttttcccaag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaaccttg tccttgc(ccc cagctttg gtgcggatca 350  
ttgtcctnat ngccagcctt gtggcctac cctacctggg ggtgcacggt 400  
gcgaccctgg gcgtgggttc ctcctggcg ggca 434

<210> 10  
<211> 154  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 49, 68, 83, 90, 98, 119  
<223> unknown base

<400> 10  
tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50  
acactgaaga aaaccttngt cttgc(cccc agntttgtgn tgccgatnat 100  
cgtcctcatc gccagcctng tggcctacc ctacctgggg gtgcacggtg 150  
agac 154

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
ctgatccggt tcttggtgcc cctg 24

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
gctctgtcac tcacgctc 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
tcatctttc cctctccc 18

<210> 14  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
ccttccgcca cggagttc 18

<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 15  
gccaaagtcc actccgatga tgtc 24

<210> 16  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
gcctgctgtg gtcacaggc tccg 24

<210> 17  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcggggagca ggccttgaac cggggcatcg ctgctgtcaa ggagg 45

<210> 18  
<211> 1901  
<212> DNA  
<213> Homo sapiens

<400> 18  
cccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50

gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100

ctctgcccccc tgcatcctgt gcagctgctg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200  
tccatcatta tgctgagccc gggcggtggag agtcagctct acaagctgcc 250  
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300  
tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc 350  
gccacggcgg ccttcttctt cttcttttc accctgctca tgctctgcgt 400  
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450  
ttaagttcct gatcctggtg ggcctcaccg tgggtgcctt ctacatccct 500  
gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggctcctt 550  
cctcttcatac ctcatccagc tggtgctgt catcgacttt gcgcactcct 600  
ggaaccagcg gtggctggc aaggccgagg agtgcgattc ccgtgcctgg 650  
tacgcaggcc tcttcttctt cactctccctc ttctacttgc tgtcgatcgc 700  
ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750  
agggcaaggt cttcatcagc ctcaacctca cttctgtgt ctgcgtgtcc 800  
atcgctgctg tcctgccc aa ggtccaggac gcccagccca actcgggtct 850  
gctgcaggcc tcggcatca ccctctacac catgtttgtc acctggtcag 900  
ccctatccag tatccctgaa cagaaatgca acccccattt gccaacccag 950  
ctgggcaacg agacagttgt ggcaggcccc gagggctatg agacccagtg 1000  
gtgggatgcc ccgagcattg tgggcctcat catttcctc ctgtgcaccc 1050  
tcttcatcag tctgcgtcc tcagaccacc ggcaggtgaa cagcctgatg 1100  
cagaccgagg agtgcccacc tatgcttagac gccacacagc agcagcagca 1150  
gcaggtggca gcctgtgagg gcccggcctt tgacaacgag caggacggcg 1200  
tcacctacag ctactccttc ttccacttct gcctggtgct ggcctcaactg 1250  
cacgtcatga tgacgctcac caactggtac aagcccggtg agacccggaa 1300  
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350  
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aacccgcact tcagctgagg cagcctcaca gcctgccatc tggtgccctcc 1450  
tgccacctgg tgcctctcg ctcggtgaca gccaacctgc cccctccccca 1500  
caccaatcag ccaggctgag ccccccaccc tgccccagct ccaggacctg 1550  
ccctgagcc gggccttcta gtcgtagtgc ctccagggtc cgaggagcat 1600

caggctcctg cagagccccca tccccccgcc acacccacac ggtggagctg 1650  
cctcttcctt cccctcctcc ctgttgccca tactcagcat ctcggatgaa 1700  
agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc 1750  
gggaaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800  
tggtcacgta ccccagggga ccctgcccccc ttccctggact tcgtgcctta 1850  
ctgagtctct aagactttt ctaataaaca agccagtgcg tgtaaaaaaaaa 1900

a 1901

<210> 19  
<211> 457  
<212> PRT  
<213> Homo sapiens

<400> 19

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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro
				20				25						30
Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe
				35				40						45
Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly
				50				55						60
Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly
				65				70						75
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser
				80				85						90
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala
				95				100						105
Ala	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	
							110		115					120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe
				125				130						135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr
				140				145						150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val
				155				160						165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile
				170				175						180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu  
185 190 195

Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr  
200 205 210

Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe  
215 220 225

Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe  
230 235 240

Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala  
245 250 255

Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu  
260 265 270

Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser  
275 280 285

Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro  
290 295 300

Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr  
305 310 315

Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile  
320 325 330

Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His  
335 340 345

Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met  
350 355 360

Leu Asp Ala Thr Gln Gln Gln Gln Gln Val Ala Ala Cys Glu  
365 370 375

Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr  
380 385 390

Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met  
395 400 405

Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met  
410 415 420

Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp  
425 430 435

Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu  
440 445 450

Leu Arg Asn Arg Asp Phe Ser  
455

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
ggcgccat cttcacgttc ttcc 24

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 21  
tcatccagct ggtgctgctc 20

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 22  
cttcttccac ttctgcctgg 20

<210> 23  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 23  
cctggcaaaa aatgcaac 18

<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 24  
caggaatgta gaaggcaccc acgg 24

<210> 25  
<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
tggcacagat cttcacccac acgg 24

<210> 26  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27  
<211> 1351  
<212> DNA  
<213> Homo sapiens

<400> 27  
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50  
ttaacctggg tcaaattgcac ggattctcac ctcgtacagt tacgctctcc 100  
cgccggcacgt ccgcgaggac ttgaagtccct gagcgctcaa gtttgcgtt 150  
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagcttc 200  
tctgttagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250  
actgccgatt cggaagtccct tgaggagcgt cagaagcggc ttccctacgt 300  
cccagagccc tattaccgg aatctggatg ggaccgcctc cgggagctgt 350  
ttggcaaaga tgaacacgag agaatttcaa aggaccttgta taatatctgt 400  
aagacggcag ctacagcagg catcattggc tgggtgtatg gggaaatacc 450  
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500  
tttatcataa ccggtttcatgat gctgtcaat ctgcacatcg tgctgccaca 550  
cgaggcttca ttcgttatgg ctggcgctgg gttggagaa ctgcagtgtt 600  
tgtgactata ttcaacacag tgaacactag tctgaatgtta taccgaaata 650  
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaaagtctt 700  
tttaggataa acgttaggcct gcgtggcctg gtggctggtg gcataattgg 750  
agccttgcgtg ggcactcctg taggaggcct gctgatggca tttcagaagt 800

acgctggta gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850  
catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900  
cctccctgag aaaattgaaa gtagttacg ggaagatgaa cctgagaatg 950  
atgctaagaa aattgaagca ctgctaaacc ttcctagaaa cccttcagta 1000  
atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050  
gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100  
tctttggta gcctgctgac aaatttaagt gctggtacct gtggtggcag 1150  
tggcttgctc ttgtctttt ctttcttt taactaagaa tggggctgtt 1200  
gtactctcac tttacttac cttaaattta aatacatact tatgtttgta 1250  
ttaatctatc aatatatgca tacatggata tatccaccca cctagattt 1300  
aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350

t 1351

<210> 28  
<211> 285  
<212> PRT  
<213> Homo sapiens

<400> 28  
Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala  
1 5 10 15  
  
Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala  
20 25 30  
  
Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val  
35 40 45  
  
Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu  
50 55 60  
  
Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala  
65 70 75  
  
Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val  
80 85 90  
  
Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile  
95 100 105  
  
Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val  
110 115 120  
  
Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly  
125 130 135

Trp Arg Trp Gly Trp Arg Thr Ala Val Phe Val Thr Ile Phe Asn  
140 145 150

Thr Val Asn Thr Ser Leu Asn Val Tyr Arg Asn Lys Asp Ala Leu  
155 160 165

Ser His Phe Val Ile Ala Gly Ala Val Thr Gly Ser Leu Phe Arg  
170 175 180

Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly Gly Ile Ile Gly  
185 190 195

Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala Phe Gln  
200 205 210

Lys Tyr Ala Gly Glu Thr Val Gln Glu Arg Lys Gln Lys Asp Arg  
215 220 225

Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg Leu  
230 235 240

Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Arg  
245 250 255

Glu Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu  
260 265 270

Asn Leu Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp  
275 280 285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150

ctacagcagg catcattggc tgggtgtatg gggaaatacc agcttttatt 200

catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250

ccggtttcatg gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300

ttcgttcatg gctggcgccg aacc 324

<210> 30

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure  
<222> 262, 330, 371  
<223> unknown base

<400> 30  
tcaagttgt ccgttaggtcg agagaaggcc atggaggtgc cgccaccggc 50  
accgcggagc tttttctgt agagcattgt gcctattcc ccgagtttt 100  
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gcggcttccc tacgtcccaag agccctatata cccggaattt ggatgggacc 200  
gcctccggga gctgttggc aaagatgaac agcagagaat ttcaaaggac 250  
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350  
agagccaggc agaaatttat nataacc 377

<210> 31  
<211> 20  
<212> DNA .  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 31  
tcgtacagtt acgctctccc 20

<210> 32  
<211> 20  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20 ..  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataaacgaatg aagcctcggt 20

<210> 34  
<211> 40  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaataatct gtaagacggc agctacagca ggcatttcattt 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

gagccgcgc cgcgcgcgc cgcgcactg cagccccagg ccccgcccc 50

ccacccacgt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100

gacaaaggcag ctgtcaggga acctccgccc gagtcgaatt tacgtgcagc 150

tgccggcaac cacaggttcc aagatggtt gcgggggctt cgcgtgttcc 200

aagaactgcc tgtgcgcctt caacctgctt tacaccttgg ttagtctgtt 250

gctaatttggaa attgctgcgt ggggcattgg cttcgggctg atttccagtc 300

tccgagtggt cggcgtggc attgcagtgg gcatcttctt gttcctgatt 350

gcttttagtgg gtctgattgg agctgtaaaa catcatcagg tggcttattt 400

tttttatatg attattctgt tacttgtatt tattgtttag ttttctgtat 450

cttgcgcctt tttagccctg aaccaggagc aacagggtca gcttctggag 500

gttgggttggaa acaatacggc aagtgcgtca aatgacatcc agagaaatct 550

aaactgctgt gggttccgaa gtgttaaccc aaatgacacc tgcgtggcta 600

gctgtgttaa aagtgaccac tcgtgcgtcg catgtgcgtcc aatcatagga 650

aatatgctg gagagggttt gagattgtt ggtggcattt gcctgttctt 700

cagttttaca gagatcctgg gtgttggct gacctacaga tacaggaacc 750

agaaagaccc ccgcgcgaat cctagtgcatt tcctttgtat agaaaacaag 800

gaagatttcc ttgcgttata tgatctgtt cactttctgt aatttctgt 850

taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900

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ggggcacct ggaatttact gtattcattt tcgggcactg tccactgtgg 1050

ccttcttag cattttacc tgcagaaaaa ctttgtatgg taccactgtg 1100

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agcactgtgc tgttagata gttcctactg gaaaaagagt gcaaattat 1200  
taaaatcaga aagtatgaga tcctgttatg ttaaggaaa tccaaattcc 1250  
caattttttt tggctttttt aggaaagatt gttgtggtaa aaagtgttag 1300  
tataaaaatg ataatttact tgtgtcttt tatgattaca ccaatgtatt 1350  
ctagaaatag ttatgtctta ggaaatttg gtttaatttt tgactttac 1400  
aggttaagtgc aaaggagaag tggttcatg aatgttcta atgtataata 1450  
acatttacct tcagcctcca tcagaatgga acgagtttg agtaatcagg 1500  
aagtatatct atatgatctt gatattgtt tataataatt tgaagtctaa 1550  
aagactgcat ttttaaacaa gttagtatta atgcgttggc ccacgttagca 1600  
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atctcccata atttgaattt gaaatcgat tttgtggctc ttatattct 1750  
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<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

Met	Val	Cys	Gly	Gly	Phe	Ala	Cys	Ser	Lys	Asn	Cys	Leu	Cys	Ala
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Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
														30
20								25						

Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
														45
35								40						

Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
														60
50								55						

Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
														75
65								70						

Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe	
														90
80								85						

Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Gl	Gln	Gly	
														105
95								100						

Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn  
110 115 120

Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn  
125 130 135

Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser  
140 145 150

Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val  
155 160 165

Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu  
170 175 180

Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp  
185 190 195

Pro Arg Ala Asn Pro Ser Ala Phe Leu  
200

<210> 37

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336

<223> unknown base

<400> 37

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tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttgg 100

tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggAAC 150

aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200

gttccgaagt gttaacccaa atgacacactg tntggcttagc tgtgttaaaa 250

gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gaggttttga gatttgttgg tggcattggc ctgttnttca gttttacaga 350

gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 27

<223> unknown base

<400> 38

aatcccaaatttcccccaattttgggncttttagggaaa gatgtgtgt 50  
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ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggttaa 150  
ttttgactt ttacaggtaa gtgcaaaggaa gaagtgggtt catgaaatgt 200  
tctaattgtat aataacattt accttcagcc tcccatcaga atgaaacgag 250  
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgtttata 300  
taatttgaag tctaaaagac tgcattttta aacaagtttag tattaatgcg 350  
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaata 400  
ccgaaaaatcat gaaagttctc agtattgtaa cagcaacttg tcaaaccctaa 450  
gcataatttga atatgatctc ccataatttggaaat cgtattgtgt 500  
ggagggaaatg gcaatcttgcgtgtgctgaa ggacacagta agagcaccaa 550  
gttgcgtcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttggtagc ccctgaaacc aggagcaaca gggncagct tcctggaggt 100  
tggttggcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150  
aatcctaaac tgctgtgggt tccgaagtgtt taacccaaat gacacctgtc 200  
tggctngctg tgtaaaaagt gaccactcgt gctgccatg tgctccaatc 250  
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40  
acccacgtct gcgttgctgc c 21

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 41  
gagaatatgc tggagagg 18

<210> 42  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 42  
aggaatgcac taggattcgc gcgg 24

<210> 43  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 43  
ggccccaaag gcaaggacaa agcagctgac agggAACCTC cgccg 45

<210> 44  
<211> 2061  
<212> DNA  
<213> Homo sapiens

<400> 44  
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gacgctgcag tgtgaggac ctgtctgcac tgaggagac agctgccaca 150  
cgaggatga cttgactgat gcaaggaaag ctggcttcca ggtcaaggcc 200  
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250  
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gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350

gatggctcag ctctgggtcc ccccgggcct aacaggaaat tctccatcac 400  
cgtggtacaa aaggcagaca gcgggcacta ccactgcagt ggcatcttcc 450  
agagccctgg tcctggatc ccagaaacag catctgttgt ggctatcaca 500  
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agctaactca cccttccacc atatgaggac gtggcaagaa gatgacatgt 1950  
atgagaacca aaaaacagct gtcgccaaac accgactctg tcgttgcctt 2000  
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ttgttagccta a 2061

<210> 45

<211> 359

<212> PRT

<213> Homo sapiens

<400> 45

Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser  
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Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe  
20 25 30

Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
35 40 45

Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
50 55 60

Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
65 70 75

Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
80 85 90

Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
95 100 105

Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
110 115 120

Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
125 130 135

Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
140 145 150

Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val  
155 160 165

Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala  
170 175 180

Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys  
185 190 195

Leu Pro Leu Gln Arg Ser Ala Ala Arg Leu Leu Phe Ser Phe Tyr  
200 205 210  
  
Lys Asp Gly Arg Ile Val Gln Ser Arg Gly Leu Ser Ser Glu Phe  
215 220 225  
  
Gln Ile Pro Thr Ala Ser Glu Asp His Ser Gly Ser Tyr Trp Cys  
230 235 240  
  
Glu Ala Ala Thr Glu Asp Asn Gln Val Trp Lys Gln Ser Pro Gln  
245 250 255  
  
Leu Glu Ile Arg Val Gln Gly Ala Ser Ser Ser Ala Ala Pro Pro  
260 265 270  
  
Thr Leu Asn Pro Ala Pro Gln Lys Ser Ala Ala Pro Gly Thr Ala  
275 280 285  
  
Pro Glu Glu Ala Pro Gly Pro Leu Pro Pro Pro Pro Thr Pro Ser  
290 295 300  
  
Ser Glu Asp Pro Gly Phe Ser Ser Pro Leu Gly Met Pro Asp Pro  
305 310 315  
  
His Leu Tyr His Gln Met Gly Leu Leu Leu Lys His Met Gln Asp  
320 325 330  
  
Val Arg Val Leu Leu Gly His Leu Leu Met Glu Leu Arg Glu Leu  
335 340 345  
  
Ser Gly His Gln Lys Pro Gly Thr Thr Lys Ala Thr Ala Glu  
350 355

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttccagcgc caattctc 18

<210> 48

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agt~~t~~ttgga ctgtatgc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaact~~t~~gggtt gtcctc~~at~~gtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
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<210> 51  
<211> 2181  
<212> DNA  
<213> Homo sapiens

<400> 51  
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gaagtagctc tggctgtat gggatctta ctgggc~~ct~~gc tactcct~~gg~~g 150  
gcacctaaca gtggacactt atggccgtcc catcct~~gg~~aa gtgccagaga 200  
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ctcagaccc~~t~~ gtcaccat~~ct~~ ttctacgt~~g~~a ctcttct~~g~~ga gaccat~~at~~cc 350  
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gatgtatccc tccaatt~~g~~ag caccct~~gg~~ag atggat~~g~~acc ggagccacta 450  
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tctaaatacc agagggaga tgcccatagc actaggactt ggtcatcatg 1950  
cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000  
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tggtgctcaa taaatatcta atcataaacag c 2181

<210> 52  
<211> 321  
<212> PRT  
<213> Homo sapiens

<400> 52  
Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val  
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Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr  
20 25 30  
  
Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
35 40 45  
  
Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
50 55 60  
  
Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
65 70 75  
  
His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
80 85 90  
  
Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
95 100 105  
  
Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
110 115 120  
  
Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
125 130 135  
  
Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
140 145 150  
  
Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
155 160 165  
  
Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
170 175 180  
  
Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr  
185 190 195

Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe  
200 205 210

Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile  
215 220 225

Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys  
230 235 240

Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser  
245 250 255

Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr  
260 265 270

Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe  
275 280 285

Ala Ile Ile Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr  
290 295 300

Met Ala Tyr Ile Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His  
305 310 315

Val Tyr Glu Ala Ala Arg  
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<210> 53

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

tatccctcca attgagcacc ctgg 24

<210> 54

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 54

gtcggaaagac atcccaacaa g 21

<210> 55

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55  
cttcacaatg tcgctgtgct gctc 24

<210> 56  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 56  
agccaaatcc agcagctggc ttac 24

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 57  
tgatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58  
<211> 2458  
<212> DNA  
<213> Homo sapiens

<400> 58  
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cgcccgac atggctgcag ccacctcgcg cgacccccga ggcgccgcgc 100  
ccagctcgcc cgaggctccgt cggaggcgcc cggccgcccc ggagccaagc 150  
agcaactgag cgggaaagcg cccgcgtccg gggatcggga tgtccctcct 200  
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cagtcaagca gaaccacacag ccttattaca cctgtctaca ccatgtactg 1800  
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ttgaaaatagt gggagatgga gaagagtgaa tgagttctc ccactctata 1950  
ctaatactcac tatttgtatt gagccaaaa taactatgaa aggagacaaa 2000  
aatttgtgac aaaggattgt gaagagctt ccatcttcat gatgttatga 2050  
ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100

cctcaaatca gatgcctcta aggacttcc tgctagatat ttctggaagg 2150  
agaaaataca acatgtcatt tatcaacgtc cttagaaaga attcttctag 2200  
agaaaaaggg atcttaggaat gctgaaagat tacccaacat accattata 2250  
tctcttcttt ctgagaaaat gtgaaaccag aattgcaaga ctgggtggac 2300  
tagaaaggg gattagatca gtttctt aatatgtcaa ggaaggttagc 2350  
cgggcatggc gccaggcacc tgttagaaaa tccagcaggt ggaggttgca 2400  
gtgagccgag attatgccat tgcactccag cctgggtgac agagcgggac 2450  
tccgtctc 2458

<210> 59  
<211> 373  
<212> PRT  
<213> Homo sapiens

<400> 59

Met Ser Leu Leu Leu Leu Leu Leu Val Ser Tyr Tyr Val Gly  
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Thr Leu Gly Thr His Thr Glu Ile Lys Arg Val Ala Glu Glu Lys  
20 25 30

Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp  
35 40 45

Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln  
50 55 60

Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu  
65 70 75

Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu  
80 85 90

Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp  
95 100 105

Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val  
110 115 120

Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro  
125 130 135

Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr  
140 145 150

Leu Gln Cys Glu Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr  
155 160 165

Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro

170	175	180
Pro Lys Ser Arg Ile Asp Tyr Asn His	Pro Gly Arg Val Leu	Leu
185	190	195
Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala	
200	205	210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val	
215	220	225
Gln Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly	
230	235	240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu	
245	250	255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Arg Pro	
260	265	270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val	
275	280	285
Lys Pro Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly		
290	295	300
Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln	
305	310	315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr	
320	325	330
Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro		
335	340	345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro	
350	355	360
Ser Met Ile Pro Ser Gln Ser Arg Ala	Phe Gln Thr Val	
365	370	

<210> 60  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 60  
ccagtgcaca gcaggcaacg aagc 24

<210> 61  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 61  
actaggctgt atgcctgggt gggc 24

<210> 62  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 62  
gtatgtacaa agcatcgca tggttgcagg agcagtgaca ggc 43

<210> 63  
<211> 3534  
<212> DNA  
<213> Homo sapiens

<400> 63  
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tctccccgcc tgggcggcct cgccgctggg caggtgctga gcgcccctag 150  
agcctccctt gccgcctccc tcctctgcgg ggccgcagca gtgcacatgg 200  
ggtgttggag gtagatgggc tcccgcccg ggaggcggcg gtggatgcgg 250  
cgctggcag aagcagccgc cgattccagc tgcccgccgc gccccggcgc 300  
cccctgcag tccccggttc agccatggg acctctccga gcagcagcac 350  
cgccctcgcc tcctgcagcc gcatgcggc ccgagccaca gccacgatga 400  
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ccagaacaga aggcctcgaa tctcattggc acataccgcc atgttgaccg 500  
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tgaggagctg cgggtgatttgcgttgcgatgc atgctccact ttctaaatcc 2200  
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ctcctggact ctgtttatag ccatcttcctt gacgtgttgcgttgcgatgc 2300

<210> 64  
<211> 655  
<212> PRT  
<213> *Homo sapiens*

<400> 64

Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser  
1 5 10 15

Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu  
20 25 30

Leu Leu Leu Gly Phe Leu Ser Thr Thr Ala Gln Pro Glu Gln  
35 40 45

Lys Ala Ser Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala  
50 55 60

Thr Gly Gln Val Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr  
65 70 75

Val Ser Glu His Cys Thr Asn Thr Ser Leu Arg Val Cys Ser Ser  
80 85 90

Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn Gly Ile Glu Lys  
95 100 105

Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met Ile Glu Lys  
110 115 120

Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys Pro Pro  
125 130 135

Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His Thr Val Cys  
140 145 150

Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr Glu Asp  
155 160 165

Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser Asp Val Pro  
170 175 180

Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys Leu Ser Gln  
185 190 195

Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn Val  
200 205 210

Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser Pro  
215 220 225

Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu  
230 235 240

Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu  
245 250 255

Ser Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile  
260 265 270

Gln Glu Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys  
275 280 285

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His  
290 295 300

Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser  
305 310 315

Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly  
320 325 330

Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp  
335 340 345

Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu  
350 355 360

Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg  
365 370 375

Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu  
380 385 390

Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu  
395 400 405

Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys  
410 415 420

Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln  
425 430 435

Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn  
440 445 450

Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His  
455 460 465

Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser  
470 475 480

Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg  
485 490 495

Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala  
500 505 510

Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser  
515 520 525

Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro  
530 535 540

Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu  
545 550 555

Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu  
560 565 570

Ser Arg Asn Gly Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val  
575 580 585

Leu Arg Gln Val Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe  
590 595 600

Asp Asp Met Leu His Phe Leu Asn Pro Glu Glu Leu Arg Val Ile  
605 610 615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu  
620 625 630

Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp  
635 640 645

Ser Val Tyr Ser His Leu Pro Asp Leu Leu  
650 655

<210> 65

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtacgcgtgc acatgggttg ttgg 24

<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

accgcacatc ctcagtctct gtcc 24

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 67

acgatgatcg cgggcctccct tctcctgcct ggattcctta gcaccaccac 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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acatttttgg gactcggaa ttatgaggtt gaggtggagg cgtagccgga 100  
tgtcagaggt cctgaaaatag tcaccatggg ggaaaatgtat ccgcctgctg 150  
ttgaagcccc cttctcatc cgatcgctt ttggccttga tgatttggaa 200  
ataagtccctg ttgcaccaga tgcagatgtt gttgctgcac agatcctgtc 250  
actgctgcca ttgaagttt ttccaatcat cgtcattggg atcattgtcat 300  
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catccactga aa 2412

<210> 69  
<211> 453  
<212> PRT  
<213> Homo sapiens

<400> 69  
Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe  
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Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala  
20 25 30  
Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro  
35 40 45  
Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile

50	55	60
Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly		
65	70	75
Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala		
80	85	90
Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr		
95	100	105
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe		
110	115	120
Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly		
125	130	135
His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr		
140	145	150
Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe		
155	160	165
Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys		
170	175	180
Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala		
185	190	195
Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg		
200	205	210
Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu		
215	220	225
Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His		
230	235	240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala		
245	250	255
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile		
260	265	270
Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His		
275	280	285
Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg		
290	295	300
Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr		
305	310	315
Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu		
320	325	330
Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala		

335 340 345

Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala  
350 355 360

Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr  
365 370 375

Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr  
380 385 390

Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val  
395 400 405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe  
410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg  
425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp  
440 445 450

Leu Lys Thr

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgatc cagcctgtgt gcctgcccaa ctctgaagag 50  
<210> 73  
<211> 3305  
<212> DNA  
<213> Homo sapiens  
  
<400> 73  
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gcagggcaca agtgtgcaga tggaaaaatc tgcctgaatc gtcaatgtca 2250  
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gaaat 3305

<210> 74  
<211> 735  
<212> PRT  
<213> Homo sapiens

<400> 74  
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20 25 30  
  
Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala  
35 40 45  
  
Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp  
50 55 60  
  
Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu  
65 70 75  
  
Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile  
80 85 90  
  
Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp  
95 100 105  
  
Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly  
110 115 120

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys  
125 130 135

Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val  
140 145 150

Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro  
155 160 165

Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His  
170 175 180

Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser  
185 190 195

Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr  
200 205 210

Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln  
215 220 225

Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu  
230 235 240

Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg  
245 250 255

Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys  
260 265 270

Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp  
275 280 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala  
290 295 300

Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met  
305 310 315

Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile  
320 325 330

Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu  
335 340 345

Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu  
350 355 360

Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys  
365 370 375

Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser  
380 385 390

Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met  
395 400 405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly  
410 415 420

Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys  
425 430 435

Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala  
440 445 450

Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu  
455 460 465

Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg  
470 475 480

Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala  
485 490 495

Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser  
500 505 510

Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr  
515 520 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro  
530 535 540

Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro  
545 550 555

Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys  
560 565 570

Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly  
575 580 585

Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr  
590 595 600

Asn Ile Pro Leu Gln Gln Gly Arg Ile Leu Cys Arg Gly Thr  
605 610 615

His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu  
620 625 630

Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln  
635 640 645

Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln  
650 655 660

Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys  
665 670 675

Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly  
680 685 690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln  
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro  
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile  
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctgacaacga aaacaaaaca gtttggggg ttcaggaggg gaantccagc 100

ctacccagga agtttgcaga aacagtgcaa ggaaggcag ganttcctgg 150

ttgagnttt tgntaaaaca tggacatgnt tcagtgctgc tcntgagaga 200

gtagcaggtt accacttttgc caggccccca gccctgcagc aaggaggaag 250

aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

agcaagggtt gggcccagtg tcccctttcc ccagtgacac ctcagccttg 350

gcagccctga taactggtn ntggctgcaa nttaatgctn tgatatggct 400

tttagcattt attatatgaa aatagcaggg tttagttt taatttatca 450

gagaccctgc cacccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

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<400> 76

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<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 77  
catgagcatg tgcacggc 18

<210> 78  
<211> 18  
<212> DNA  
<213> Artificial Sequence

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<400> 78  
tacctgcacg atgggcac 18

<210> 79  
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<400> 79  
cactggcac ctcccttc 18

<210> 80  
<211> 26  
<212> DNA  
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<220>  
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<400> 80  
ctccaggctg gtctccaagt cttcc 26

<210> 81  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 81  
tccctgttgg actctgcagc ttcc 24

<210> 82  
<211> 19  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 82  
cttcgctggg aagagttt 19

<210> 83  
<211> 50  
<212> DNA  
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<220>  
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<400> 83  
gtgcaaccaa cagatacAAA ctcttcccAG cgaagaAGCT gaaaAGCGTC 50 .

<210> 84  
<211> 1714  
<212> DNA  
<213> Homo sapiens

<400> 84  
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gttagagatgg gatttcaccg tgTTAGCCAG gattgtctca atctgacCTC 100  
atgatctgcc cgccTcggcc tcccaaAGTG ctgggattAC aggCGAGTGC 150  
aaccacacCC ggCCacAAAC ttTTAAGAA gttaATgAAA ccatacCTT 200  
tacatTTTA atgacaggAA aATgCTcaca ataattgtTA accCAAAATT 250  
ctggatacaa aagtacaATC ttTactgtGT aaatacatgt atatgtACTA 300  
tatgAAAATA tacCAAATAT caataACT tatctCTGGG taAAAACCTC 350  
ttCTCataACC ctgtGctaAC aactTTAAC AAAAATTG catcaCTTT 400  
aagaatcaag AAAAATTCT gaaggTCATA TgggacAGAA AAAAAGACCA 450  
aggaaaaat cacGCCACTT gggAAAAAAA gattcgAAAT CTGCCTTTT 500  
atagatttGT aattaATAAG gtccaggCtt tctaAGcaAC ttaaatgtTT 550  
tgTTTcgAAA caaAGTACTT gtctggatgt aggAGGAAG ggAGTgATgt 600  
cactGCCATT atgatGCCc TTGAATATAA gaccCTACTT gCTatCTCCC 650  
ctgcaccAGC caggAGCCAC CCATCCTCCA gcACACTGAG cAGCAAGCTG 700  
gacacacGGC acACTGATCC AAATGGGtaA gggatggTG gCGATGCTCA 750  
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tttGTTcCTT TAACCAGTAT GCCGGAAGCT ACTGCAGCCG AAACCAACAA 850  
GCCCTCCAAC agtGCCCTAC AGCCTACAGC CGGTCTCCTT GTGGTCTTGC 900

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<210> 85

<211> 67

<212> PRT

<213> Homo sapiens

<400> 85

Met Gly Lys Gly Met Val Ala Met Leu Ile Leu Gly Leu Leu Leu  
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Leu Ala Leu Leu Leu Pro Val Gln Val Ser Ser Phe Val Pro Leu  
20 25 30

Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser  
35 40 45

Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu  
50 55 60

Ala Leu Leu His Leu Tyr His  
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<210> 86

<211> 23

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 86  
acgggcacac tggatcccaa atg 23

<210> 87  
<211> 29  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 87  
ggtagagatg tagaaggca agcaagacc 29

<210> 88  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 88  
gctccctacc cgtcaggtt ttttcatttg ttcccttaac cagtatgccg 50

<210> 89  
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<212> DNA  
<213> Homo sapiens

<400> 89  
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gctgctgctg ggccatggcg gcggcggcg ctggggcgcc cggccggcagg 150  
aggcggcggc ggcggcggcg gacggggccc ccgcggcaga cggcgaggac 200  
ggacaggacc cgcacagcaa gcacctgtac acggccgaca tgttcacgca 250  
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aacagcatgg aagatgccaa agtctatgtg gctaaagtgg actgcacggc 400  
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ttttaa 2956

<210> 90  
<211> 432  
<212> PRT  
<213> Homo sapiens

<400> 90  
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35 40 45

Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro  
50 55 60

His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile  
65 70 75

Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly  
80 85 90

His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys  
95 100 105

Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp  
110 115 120

Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly  
125 130 135

Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys  
140 145 150

Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu  
155 160 165

Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu  
170 175 180

Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser  
185 190 195

Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His Phe Ile  
200 205 210

Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro  
215 220 225

Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val  
230 235 240

Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser  
245 250 255

Gly Asn Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp  
260 265 270

Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser  
275 280 285

Leu Arg Glu Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly  
290 295 300

Ala Thr Glu Thr Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala  
305 310 315

Glu Pro Glu Ala Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn  
320 325 330

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe  
335 340 345  
Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp  
350 355 360  
Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys  
365 370 375  
Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys  
380 385 390  
Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly  
395 400 405  
Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu  
410 415 420  
His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu  
425 430

<210> 91  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 91  
atgttcttcg cgccctggtg 20

<210> 92  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
ccaagccaaac acactctaca g 21

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
aagtggtcgc ctttgcaac gtgc 24

<210> 94  
<211> 23

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
ggtcaaagg gatatatcgc cac 23

<210> 95  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 95  
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccc 49

<210> 96  
<211> 1016  
<212> DNA  
<213> Homo sapiens

<400> 96  
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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150  
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agagtgccat cttaccatgt actttgtctg tgagttcatc aagaagaaaa 850  
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aaaaaaaaaaa aaaaaaa 1016

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<210> 97  
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<212> PRT  
<213> Homo sapiens

<400> 97

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Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile  
20 25 30

Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser  
35 40 45

Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu  
50 55 60

Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
65 70 75

Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys  
80 85 90

Thr Gly Pro Ile Gly Lys Gly Asp Lys Gly Glu Lys Gly Leu  
95 100 105

Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp  
110 115 120

Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile  
125 130 135

Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala  
140 145 150

Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu  
155 160 165

Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly  
170 175 180

Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile  
185 190 195

Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn			
215	220	225	
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser			
230	235	240	
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly			
245	250	255	
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys			
260	265	270	
Glu Phe Ile Lys Lys Lys Lys			
275			

<210> 98  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 98  
cgctgactat gttgccaaga gtgg 24

<210> 99  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe .

<400> 99  
gatgatggag gctccataacc tcag 24

<210> 100  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 100  
gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101  
<211> 2574  
<212> DNA  
<213> Homo sapiens

<400> 101  
ggttctatcg attcgaattc ggccacactg gccggatcct ctagagatcc 50

ctcgacctcg acccacgcgt ccgctgctct ccgcccgtgt ggagtggtgg 100  
ggccctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150  
gagaagtctc agctagaacg agcggcccta ggtttcgga agggaggatc 200  
agggatgtt gcgagcggct ggaaccagac ggtgccata gaggaagcgg 250  
gctccatgac tgccctcctg ctgctgcccc tgctgctgtt gctaccgctg 300  
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cttggccttt gcgggtgcgag ctctgtctg caaaaagggt cttcgagctc 400  
gcgcgcctggc cgccgcgtgcc gccgaccggg aagggtccga ggggggctgc 450  
agcctggcct ggcgcctcgc ggaactggcc cagcagcgcg ccgcgcacac 500  
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gctctggttc gggctggcca aggccggcct ggcactgcc tttgtgcccc 850  
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ggtgtccacc aggaagatgt gatctacccct gcgcgcgcgc tctaccacat 1250  
gtccgggttcc ctgctggca tcgtggcgtg catggcatt gggccacag 1300  
tggtgctgaa atccaagttc tcggctggc agttctggaa agattgccag 1350  
cagcacaggg tgacgggtttt ccagtttccat ggggagctgt gccgataacct 1400  
tgtcaaccag ccccccggca aggcagaacg tggccataag gtccggctgg 1450

cagtggcag cgggctgcgc ccagataacct gggagcggtt tgtgcggcgc 1500  
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gaccccaa cagcagaaag ttcggatggc aaatgagggc ttcgacccca 2200  
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catggcccaa cttgtttatt gcag 2574

<210> 102  
<211> 730  
<212> PRT  
<213> Homo sapiens

<400> 102  
Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser  
1 5 10 15  
Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly  
20 25 30

Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala  
35 40 45

Gly Ser Met Ala Ala Leu Leu Leu Pro Leu Leu Leu Leu Leu  
50 55 60

Pro Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp  
65 70 75

Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys  
80 85 90

Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro  
95 100 105

Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu  
110 115 120

Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser  
125 130 135

Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala  
140 145 150

Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp  
155 160 165

Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala  
170 175 180

Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe  
185 190 195

Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Ala Ala Ala Pro  
200 205 210

Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly Pro  
215 220 225

Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg  
230 235 240

Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His  
245 250 255

Cys Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu  
260 265 270

Phe Leu Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met  
275 280 285

Gly Leu His Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly  
290 295 300

Ile Ser Asp Leu Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro  
305 310 315

Val Pro Gly Tyr Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys  
320 325 330

Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala  
335 340 345

Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln  
350 355 360

Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro  
365 370 375

Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met  
380 385 390

Gly Ile Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly  
395 400 405

Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln  
410 415 420

Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser  
425 430 435

Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly Ser Gly  
440 445 450

Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro  
455 460 465

Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala  
470 475 480

Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser  
485 490 495

Trp Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp  
500 505 510

Val Thr Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met  
515 520 525

Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser  
530 535 540

Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala  
545 550 555

Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe  
560 565 570

Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu  
575 580 585

Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu  
590 595 600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp  
605 610 615

Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His  
620 625 630

Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His  
635 640 645

Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu  
650 655 660

Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu  
665 670 675

Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn  
680 685 690

Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu  
695 700 705

Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr  
710 715 720

Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile  
725 730

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctccacc tg 22

<210> 104

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 104

ggagaatgtg gccacaac 18

<210> 105

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105  
gccctggcac agtgactcca tagacg 26

<210> 106  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 106  
atccacttca gcggacac 18

<210> 107  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 107  
ccagtgcag gataacctctc ttccccccag agcataacag acacg 45

<210> 108  
<211> 2579  
<212> DNA  
<213> Homo sapiens

<400> 108  
cctgtttaa gctgaggttt cccctagatc tcgtatatcc ccaacacata 50  
cctccacgca cacacatccc caagaacctc gagtcacac caacagacac 100  
acgcgcgcac acacactcgc tctcgcttgt ccataccct cccgggggag 150  
ccggcgcgcg ctccccac ttgcgcacac tccggcgagc cgagcccgca 200  
gcgcgtccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250  
atggtggttt tttaaacact tctttccctt ctcttcctcg ttttattgc 300  
accgtttcca tctggggct agaggagcaa ggcagcagcc ttcccagcca 350  
gccctgttg gcttgccatc gtccatctgg cttataaaag tttgctgagc 400  
gcagtccaga gggctgcgct gtcgtcccc tcggctggca gaagggggtg 450  
acgctgggca gcggcgagga gcgcgcgcgt gcctctggcg ggcttcggc 500  
ttgaggggca aggtgaagag cgcaccggcc gtggggttta ccgagctgga 550  
tttgtatgtt gcaccatgcc ttcttgatc gggctgtga ttcttcccct 600  
cttggggctg ctgctctccc tccccgcccgg ggcggatgtg aaggctcgga 650

gctgcggaga ggtccgccag gcgtacggtg ccaaggatt cagcctggcg 700  
gacatcccct accaggagat cgccagggaa cacttaagaa tctgtcctca 750  
ggaatataca tgctgcacca cagaaatgga agacaagtta agccaacaaa 800  
gcaaactcga atttggaaaac cttgtggaag agacaagcca ttttgtgcgc 850  
accacttttgc tgtccaggca taagaaattt gacgaatttt tccgagagct 900  
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ccgcgccttc attgctgcca ggacctttgt ccagggctg actgtgggca 1250  
gagaagttgc aaaccgagtt tccaagggtca gcccaacccc agggtgtatc 1300  
cgtgccctca tgaagatgct gtactgccca tactgtcggt ggcttccac 1350  
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ggacccgata gatgtcaaga tttctgaagc cattatgaac atgcaagaaaa 1550  
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caagcttggaa ccggctggtc acagacataa aagagaaatt gaagctctct 1750  
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ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550  
gtgagggttt ttttttctc atttaaaat 2579

<210> 109  
<211> 555  
<212> PRT  
<213> Homo sapiens

<400> 109  
Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu  
1 5 10 15  
  
Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys  
20 25 30  
  
Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala  
35 40 45  
  
Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys  
50 55 60  
  
Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu  
65 70 75  
  
Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu Thr  
80 85 90  
  
Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe  
95 100 105  
  
Asp Glu Phe Phe Arg Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu  
110 115 120  
  
Asn Asp Met Phe Val Arg Thr Tyr Gly Met Leu Tyr Met Gln Asn  
125 130 135  
  
Ser Glu Val Phe Gln Asp Leu Phe Thr Glu Leu Lys Arg Tyr Tyr  
140 145 150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp  
155 160 165

Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr  
170 175 180

His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp  
185 190 195

Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln  
200 205 210

Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu  
215 220 225

Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro  
230 235 240

Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro  
245 250 255

Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys  
260 265 270

Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp  
275 280 285

Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu  
290 295 300

Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile  
305 310 315

Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser  
320 325 330

Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys  
335 340 345

Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe  
350 355 360

Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr  
365 370 375

Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu  
380 385 390

Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr  
395 400 405

Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu  
410 415 420

Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile  
425 430 435

Met Asn Asp Gly Leu Thr Asn Gln Ile Asn Asn Pro Glu Val Asp  
440 445 450  
Val Asp Ile Thr Arg Pro Asp Thr Phe Ile Arg Gln Gln Ile Met  
455 460 465  
Ala Leu Arg Val Met Thr Asn Lys Leu Lys Asn Ala Tyr Asn Gly  
470 475 480  
Asn Asp Val Asn Phe Gln Asp Thr Ser Asp Glu Ser Ser Gly Ser  
485 490 495  
Gly Ser Gly Ser Gly Cys Met Asp Asp Val Cys Pro Thr Glu Phe  
500 505 510  
Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg  
515 520 525  
Glu Val Asp Ser Ser Ala Ala Gln Arg Gly His Ser Leu Leu Ser  
530 535 540  
Trp Ser Leu Thr Cys Ile Val Leu Ala Leu Gln Arg Leu Cys Arg  
545 550 555

<210> 110

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

aagcgtgaca gcgggcacgt c 21

<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgccctg 40

<210> 113  
<211> 4649  
<212> DNA  
<213> Homo sapiens

<400> 113  
cgacgcgtg ggcggacgct tggcaaaag aactcggagt gccaaagcta 50  
aataagtttag ctgagaaaac gcacgcgtt tgcaagccct ggcgggttg 100  
cgccaactac gcaaagacca agcggctcc gcgcggaccg gccgcggggc 150  
tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200  
tgctgccccg agtttctgcg gaggtggagg gagatcagga aacggcttct 250  
tcctcacttc gccgcctggt gagtgcggg gagattggca aacgcctagg 300  
aaaggactgg ggaaaatagc cctggaaag tggagaaggt gatcaggagg 350  
ccggccact acggcagttt atctgtctga tcagagccag acgcgcgcg 400  
tccacttcgc agtttttcc aggtgtgggg accgcaggac agacggccga 450  
tcccggccct ctccgtacca gcactcccag gagagtcaag ctcgctcccc 500  
aacgtcgagg gcgcgttggc cacgaaaagt tcctgtccac tgtgattctc 550  
aattccttgc ttgggttttt tctccagaga actttgggt ggagatatta 600  
acttttttct tttttttttt ctttgttggaa agctgtctta gggagggggg 650  
aggaggagga gaaagtgaaa tgtgtggag aagagcgagc cttcccttgtt 700  
cttccggagt cccatccatt aagccatcac ttcttggaa ttaaagttgt 750  
cgacatggt gacagctgag aggaggagg gatttcttgc caggtggaga 800  
gtcttcaccg tcttgtgggt gcatgtgtgc gcccgcagcg gcgcggggcg 850  
cgtggttctc cgcgtggagt ctcacctggg acctgagtga atggctccca 900  
ggggctgtgc ggggcatccg cttccgcctt ctccacaggc ctgtgtctgt 950  
cctggaaaga tgcttagcaat gggggcgctg gcaggattct ggatcctctg 1000  
cctcctcaact tatggttacc tgtcctgggg ccaggcctta gaagaggagg 1050  
aagaagggc cttacttagct caagctggag agaaactaga gcccagcaca 1100  
acttccacct cccagccccca tctcattttc atcctagcgg atgatcaggg 1150  
attttagagat gtgggttacc acggatctga gattaaaaca cctactcttgc 1200  
acaagctcgc tgccgaagga gttaaactgg agaactacta tgtccagcct 1250

atttgcacac catccaggag tcagtttatt actggaaagt atcagataca 1300  
caccggactt caacattcta tcataagacc tacccaaccc aactgtttac 1350  
ctctggacaa tgccacccta cctcagaaac tgaaggaggt tggatattca 1400  
acgcatatgg tcggaaaatg gcacttggtt tttaacagaa aagaatgcat 1450  
gccaccaga agaggattt gatcacccctt tggtccctt ttgggaagt 1500  
gggattacta tacacactac aaatgtgaca gtcctggat gtgtggctat 1550  
gacttgtatg aaaacgacaa tgctgcctgg gactatgaca atggcatata 1600  
ctccacacag atgtacactc agagagtaca gcaaatttta gcttcccata 1650  
accccacaaa gcctatattt ttatatactg cctatcaagc tgttcattca 1700  
ccactgcaag ctcctggcag gtatttcgaa cactaccgat ccattatcaa 1750  
cataaacagg agaagatatg ctgccccatg ttcctgctta gatgaagcaa 1800  
tcaacaacgt gacattggct ctaaagactt atggtttcta taacaacagc 1850  
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tatggatct ggaacactgc aatccagtca gccatcagag tgcagcactg 2250  
gaaattgctt acaggaaatc ctggctacag cgactgggtc cccccctcagt 2300  
cttcagcaa cctgggaccg aaccgggtggc acaatgaacg gatcaccttg 2350  
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<210> 114  
<211> 515  
<212> PRT  
<213> Homo sapiens

<400> 114  
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Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu  
20 25 30  
Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser  
35 40 45  
Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala  
50 55 60  
Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln  
65 70 75  
Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
80 85 90  
Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys  
95 100 105  
Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro  
110 115 120  
Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln  
125 130 135  
Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro  
140 145 150

Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys  
155 160 165

Glu Val Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly  
170 175 180

Phe Asn Arg Lys Glu Cys Met Pro Thr Arg Arg Gly Phe Asp Thr  
185 190 195

Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr His Tyr  
200 205 210

Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu Asn  
215 220 225

Asp Asn Ala Ala Trp Asp Tyr Asn Gly Ile Tyr Ser Thr Gln  
230 235 240

Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro  
245 250 255

Thr Lys Pro Ile Phe Leu Tyr Thr Ala Tyr Gln Ala Val His Ser  
260 265 270

Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile  
275 280 285

Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu  
290 295 300

Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly  
305 310 315

Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly  
320 325 330

Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys  
335 340 345

Gly Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His  
350 355 360

Ser Pro Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val  
365 370 375

His Ile Thr Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly  
380 385 390

Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu  
395 400 405

Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His  
410 415 420

Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln  
425 430 435

Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu  
440 445 450

Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr  
455 460 465

Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly  
470 475 480

Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe  
485 490 495

Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr  
500 505 510

Gly Ile Gln Glu Ser  
515

<210> 115

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 115

cccaaccaa ctgttacctt ctgg 24

<210> 116

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 116

ctctctgagt gtacatctgt gtgg 24

<210> 117

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<220>

<221> unsure

<222> 33

<223> unknown base

<400> 117

gccaccctac ctcagaaact gaaggaggtt ggntattcaa cgcatatgg 50

cg<sup>g</sup> 53

<210> 118  
<211> 2260  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086  
<223> unknown base

<400> 118  
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gggctcagga ggaggaagga ggaccgcgtgc gagaatgcct ctgccctgga 150  
gccttgcgtcccgcgtctg ctctcctggg tggcaggtgg tttcgaaac 200  
gcggccagtgc aaggcatca cgggttgtta gcatcgac gtcagcctgg 250  
ggtctgtcac tatgaaacta aactggcctg ctgctacggc tggagaagaa 300  
acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttgg 350  
gagtgcgtgg gaccaaacaa atgcagatgc tttccaggat acaccggaa 400  
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aacacagatg tgtgaataaca cacggaaagct acaagtgc ttgcctcagt 500  
ggccacatgc tcataccaga tgctacgtgt gtgaactcta ggacatgtgc 550  
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gcctgtgtcc atcctcagga ctccgcctgg ccccaaatgg aagagactgt 650  
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aagatgtgtg aacacatttg gaagctacta ctgcaaatgt cacattgg 750  
tcgaactgca atatatcagt ggacgatatg actgtataga tataaatgaa 800  
tgtactatgg atagccatac gtgcagccac catgccaatt gcttcaatac 850  
ccaagggtcc ttcaagtgtta aatgcaagca gggatataaa ggcaatggac 900  
ttcgggtttc tgctatccct gaaaattctg tgaaggaagt cctcagagca 950  
cctggtagcca tcaaagacag aatcaagaag ttgcttgctc aaaaaacag 1000  
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catagaggag cgaaggcctgc gaggagatgt gttttccct aaggtgaatg 1250  
aagcaggtga attcggcctg attctggtcc aaaggaaagc gctaacttcc 1300  
aaacttggAAC ataaagattt aaatatctcg gttgactgca gcttcaatca 1350  
tgggatctgt gactggAAAC aggatagaga agatgatttt gactggaatc 1400  
ctgctgatcg agataatgct attggcttct atatggcagt tccggccttg 1450  
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gcaaccccaa agcaacttct gtttgctctt tgattaccgg ctggccggag 1550  
acaaagtcgg gaaacttcga gtgttgtga aaaacagtaa caatgccctg 1600  
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actatctta tatttgactt tgtatgtca tagccctggtt tttttgatata 1850  
tgcatcatag gacctctggc attttagaat tactagctga aaaattgtaa 1900  
tgtaccaaca gaaatattat tgtaagatgc ctttctgtta taagatatgc 1950  
caatatttgc tttaaatatc atatcactgt atcttctcag tcatttctga 2000  
atctttccnc attatattat aaaatntgga aangtcagtt tatctccct 2050  
cctcngtata tctgatttgt atangtangt tgatngcctt ctctctacaa 2100  
catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150  
ctcttatgat acttcttgaa aactatgaca tcaaagatag actttgcct 2200  
aagtggctta gctgggtctt tcatagccaa acttgtatata ttaattctt 2250  
gtaataataa 2260

<210> 119  
<211> 338  
<212> PRT  
<213> Homo sapiens

<400> 119  
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Ser Trp  
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Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His Gly  
20 25 30

Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr  
35 40 45

Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val  
50 55 60

Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val  
65 70 75

Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr  
80 85 90

Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys  
95 100 105

Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys  
110 115 120

Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser  
125 130 135

Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr  
140 145 150

Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu  
155 160 165

Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser  
170 175 180

Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe  
185 190 195

Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr  
200 205 210

Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met  
215 220 225

Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln  
230 235 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly  
245 250 255

Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu  
260 265 270

Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala  
275 280 285

His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr  
290 295 300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro  
305 310 315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly  
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys  
335

<210> 120  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 120  
cctcagtggc cacatgctca tg 22

<210> 121  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 121  
ggctgcacgt atggctatcc atag 24

<210> 122  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 122  
gataaaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123  
<211> 1199  
<212> DNA  
<213> Homo sapiens

<400> 123  
gggagctgct gctgtggctg ctggtgctgt gcgcgcgtgct cctgctcttg 50  
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ggcccgagtgg caggagcacac gcccagaatg ggagctgact gatatggtgg 150  
tgtgggtgac tggagcctcg agtggaaattg gtgaggagct ggcttaccag 200  
ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcatga 250

gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat taaaaagaaa 300  
aagatatact tgtttgccc cttgacactga ccgacactgg ttcccatgaa 350  
gcggctacca aagctgtct ccaggagttt ggtagaatcg acattctgg 400  
caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450  
atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500  
acaaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550  
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actgtgctag caagcatgct ctccggggtt ttttaatgg cttcgaaca 650  
gaacttgcca cataccagg tataatagtt tctaacattt gcccaggacc 700  
tgtgcaatca aatattgtgg agaattccct agctggagaa gtcacaaaga 750  
ctataggcaa taatggagac cagtcccaca agatgacaac cagtcgttgt 800  
gtgcggctga tgttaatcag catggccaat gattgaaag aagtttggat 850  
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cctggccctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950  
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aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050  
aatggaaaac atgaaaacag caatcttctt atgcttctga ataatcaaag 1100  
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gaatgaaata aaaaataaaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124  
<211> 289  
<212> PRT  
<213> Homo sapiens

<400> 124  
Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu  
1 5 10 15  
Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser  
20 25 30  
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu  
35 40 45  
Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu  
50 55 60

Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val  
65 70 75

Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly  
80 85 90

Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr  
95 100 105

Arg Lys Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr  
110 115 120

Lys Cys Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile  
125 130 135

Val Thr Val Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser  
140 145 150

Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn  
155 160 165

Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser  
170 175 180

Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu Asn Ser  
185 190 195

Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asp Gln  
200 205 210

Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile  
215 220 225

Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro  
230 235 240

Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala  
245 250 255

Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe  
260 265 270

Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys  
275 280 285

Thr Lys His Asp

<210> 125  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19  
<210> 126  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 126  
ctgtgaatag catcctggg 19  
  
<210> 127  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 127  
cttttcaagc cactggaggg 20  
  
<210> 128  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 128  
ctgttagacat ccaagctggc atcc 24  
  
<210> 129  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 129  
aagagtctgc atccacaccca ctc 23  
  
<210> 130  
<211> 46  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 130  
acctgacgct actatgggcc gagtgccagg gacgacgccc agaatg 46

<210> 131  
<211> 2365  
<212> DNA  
<213> Homo sapiens

<400> 131  
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ggcagggggtt tcgggctggt ggagcatgtg ctggacagg acagcatcct 100  
caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150  
tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200  
tccctggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250  
cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300  
tgagcctgat gtggctcagt ttccggaagg tccaagaacc ccagggcaag 350  
gctaagaggc actgagccct caacccaagc caggctgacc tcatactgctt 400  
tgctttggtc ttcaagccgc tcagcgtgcc tgtggacagc gtggccccgg 450  
cccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500  
aggccagtgt gaggaggcaa ggagcccaca tctgcagcgg ctccctggtg 550  
gcagacacccctt gggccctcac tgctgcccac tgcttgaaa aggccagcgc 600  
aacagaactg aattcctggt cagtggctct gggttctctg cagcgtgagg 650  
gactcagccc tggggccgaa gaggtggggg tggctgccct gcagttgccc 700  
agggcctata accactacag ccagggctca gacctggccc tgctgcagct 750  
cgcccacccc acgacccaca caccctctg cctggcccaag cccgcccatac 800  
gtttccctt tggagcctcc tgctggcca ctggctggta tcaggacacc 850  
agtgtatgctc ctgggaccct acgcaatctg cgcctgcgtc tcatacgtcg 900  
ccccacatgt aactgtatct acaaccagct gcaccagcga cacctgtcca 950  
acccggcccg gcctgggatg ctatgtgggg gccccagcc tggggtgccag 1000  
ggccctgtc agggagattc cggggccct gtgctgtgcc tcgagcctga 1050  
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cccgagatg agtgtatgagg acagctgtgt agcctgtgga tccttgagga 1250  
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ctgatgcacc agggacagct ggcctgtggc ggagccctgg tgcagagga 1350  
ggcggtgcta actgctgccc actgcttcat tggcgccag gccccagagg 1400  
aatggagcgt agggctgggg accagaccgg aggagtgggg cctgaagcag 1450  
ctcatcctgc atggagccta cacccaccct gaggggggct acgacatggc 1500  
cctcctgctg ctggcccagc ctgtacact gggagccagc ctgcggcccc 1550  
tctgcctgcc ctatcctgac caccacctgc ctgatgggga gcgtggctgg 1600  
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gcccgtgacc ctcctggggc cttagggcctg cagccggctg catgcagctc 1700  
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cctccttac tcttcagat acaatcacgc cagccacgtt gtttgaaaa 2300  
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tgttacaaaa taaaa 2365

<210> 132  
<211> 571  
<212> PRT  
<213> Homo sapiens

<400> 132  
Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu  
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Ala Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys  
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Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe  
35 40 45

Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn  
50 55 60

Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln  
65 70 75

Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val  
80 85 90

Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu  
95 100 105

Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu  
110 115 120

Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro  
125 130 135

Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu  
140 145 150

Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln  
155 160 165

Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly  
170 175 180

Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu  
185 190 195

Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn  
200 205 210

Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met  
215 220 225

Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly  
230 235 240

Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp  
245 250 255

Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu  
260 265 270

Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp  
275 280 285

Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro  
290 295 300

Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly  
305 310 315

Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp  
320 325 330

Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly  
335 340 345

Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His Cys  
350 355 360

Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly  
365 370 375

Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly  
380 385 390

Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met Ala Leu Leu Leu  
395 400 405

Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg Pro Leu Cys  
410 415 420

Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg Gly Trp  
425 430 435

Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu Gln  
440 445 450

Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu  
455 460 465

His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met  
470 475 480

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu  
485 490 495

Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu  
500 505 510

Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg  
515 520 525

Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser  
530 535 540

Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu  
545 550 555

Ala Glu Pro Gly Ser Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser  
560 565 570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133  
cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134  
tggggcagca gtttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135  
ggctggcatc atcagcttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136  
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ggggcagcct tccaccacgg ggagcccgac tgtcagccgc ctcacaggaa 150  
gatgctgcgt cggcggggca gccctggcat gggtgtgcat gtgggtgcag 200  
ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250  
cctgaagacc cagtggtggc actgggtggc accgatgcca ccctgtgctg 300  
ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350  
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gaccaggcgca ggcgcctatgc caaccgcacg gccctttcc cggacctgct 450  
ggcacaggcgca aacgcattccc tgaggctgca ggcgcgtgcgt gtggcggacg 500  
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gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850  
atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900  
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attttgggaa aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly  
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Ala Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu  
20 25 30

Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp  
35 40 45

Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu  
50 55 60

Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu  
65 70 75

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala  
80 85 90

Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala  
95 100 105

Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe  
110 115 120

Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser  
125 130 135

Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu  
140 145 150

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys  
155 160 165

Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp  
170 175 180

Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met  
185 190 195

Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val  
200 205 210

Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro  
215 220 225

Val Leu Gln Gln Asp Ala His Xaa Ser Val Thr Ile Thr Gly Gln  
230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu  
245 250 255

Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys  
260 265 270

Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala  
275 280 285

Glu Asp Gln Asp Gly Glu Gly Glu Ser Lys Thr Ala Leu Gln  
290 295 300

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile  
305 310 315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacacctat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

gctgtctgtc tgtctcattt 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 141  
tgcgaaccag gcagctgtaa gtgc 24

<210> 142  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 142  
tggaagaaga gggtggtgat gtgg 24

<210> 143  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 143  
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144  
<211> 2336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1620, 1673  
<223> unknown base

<400> 144  
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tacgttctta aatctatgaa gtcgaggagc ct ttcgctgc tttttaggg 150  
acttcttcc ttgcttcagc aacatgaggc ttttcttgc gaa cgcggc 200  
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aaggagggga tttgatgtt g tccactatg aaggctactt agaaaaggac 350  
ggctccttat ttcactccac tcacaaacat aacaatggc agcccattt 400

gtttaccctg ggcatcctgg aggctctcaa aggttggac cagggcttga 450  
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aagacaaaga tgggttata tctgccagag aatttacata taaacacgt 800  
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tgcttggtttt ttatTTTT tatATTTT ctgactccta ttAAAGAAC 950  
cccttaggtt tctaagtacc catttcttc tgataagtta ttggaaagaa 1000  
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caactggaa tataccacga catgagacca gttatagca caaattagca 1150  
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gcagctacta ttgaataaaat acctatcctg gatttt 2336

<210> 145  
<211> 211  
<212> PRT  
<213> Homo sapiens

<400> 145  
Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr  
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Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu  
20 25 30  
Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly  
35 40 45  
Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly  
50 55 60  
Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile  
65 70 75  
Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln  
80 85 90  
Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile  
95 100 105  
Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro  
110 115 120  
Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg  
125 130 135  
Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn  
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys  
155 160 165  
Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His  
170 175 180  
Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys  
185 190 195  
Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu  
200 205 210  
Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 146

ctttccttgc ttcagcaaca tgaggc 26

<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

gcccgagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

gtggaacgcg gtcttgactc tgttcgtcac ttcttgatt ggggcttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

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cagagatgcc tggctacctc gccctgcctt cagcctcacf gggctcagtc 200  
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cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100  
tgagccccggg aagcagaggt tgcagtgaac tgagatagtg atagtgccac 2150  
tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaaa 2196

<210> 150  
<211> 215  
<212> PRT  
<213> Homo sapiens

<400> 150  
Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr  
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Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met  
20 25 30  
Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp  
35 40 45  
Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His  
50 55 60  
Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys  
65 70 75  
Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu  
80 85 90  
Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro  
95 100 105  
Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu

	110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg			
	125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu			
	140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser			
	155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val			
	170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp			
	185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro			
	200	205	210
Asp Asp Gly Ala Lys			
	215		
<210> 151			
<211> 524			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> unsure			
<222> 103, 233			
<223> unknown base			
<400> 151			
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ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150			
gccctgcctt cagcctcacg gggctcagtc tcttttctc tttggtgcca 200			
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gatgtgtcgg tcatgtcgag aaacgtgcag ccggaggatg aggggattta 500			
caactgctac atcatgaacc cccc 524			
<210> 152			

<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
tcacggggct catcttttt tctcttttgtt gcccaccagg acggagcatg 50  
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cctgcctgc accttcaact ccngctacac agtgaaccac aaacagttct 150  
ccctgaactg gatttaccag gagtgcaaca actggctctg aggagatgtt 200  
cctccagttc ccgcattggaa gatcatattaa cctgaaaagct ggaagcggtt 250  
ttcaagaacc gcgtggaagt ttctcaggaa accccagcaa gtacgatgtg 300  
tcggtgatgc tgagaaacgt gcagccggag gatgaggggta tttacaactg 350  
ctacatcatg aacccccc 368

<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 153  
acggagcatg gaggtccaca gtac 24

<210> 154  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
gcacgtttct cagcatcacc gac 23

<210> 155  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 155

cgccctgcctc gcaccccaa ctcctgctac acagtgaacc acaaacagtt 50  
<210> 156  
<211> 2680  
<212> DNA  
<213> Homo sapiens  
  
<400> 156  
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atgctgtaaa aaaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp  
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Gly Leu Leu Phe Leu Leu Leu Leu Met Leu Leu Ala Asp Pro  
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Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly  
35 40 45

Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val  
50 55 60

Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile  
65 70 75

Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp  
80 85 90

Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr  
95 100 105

Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys  
110 115 120

Thr Phe Ser Leu Glu Phe Leu Asp Pro Ser Lys Ser Ser Val Gly  
125 130 135

Ser Tyr Phe His Thr Met Val Glu Ser Leu Val Gly Trp Gly Tyr  
140 145 150

Thr Arg Gly Glu Asp Val Arg Gly Ala Pro Tyr Asp Trp Arg Arg  
155 160 165

Ala Pro Asn Glu Asn Gly Pro Tyr Phe Leu Ala Leu Arg Glu Met  
170 175 180

Ile Glu Glu Met Tyr Gln Leu Tyr Gly Gly Pro Val Val Leu Val  
185 190 195

Ala His Ser Met Gly Asn Met Tyr Thr Leu Tyr Phe Leu Gln Arg  
200 205 210

Gln Pro Gln Ala Trp Lys Asp Lys Tyr Ile Arg Ala Phe Val Ser  
215 220 225

Leu Gly Ala Pro Trp Gly Gly Val Ala Lys Thr Leu Arg Val Leu  
230 235 240

Ala Ser Gly Asp Asn Asn Arg Ile Pro Val Ile Gly Pro Leu Lys

	245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu			
260	265	270	
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr			
275	280	285	
Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln			
290	295	300	
Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu			
305	310	315	
Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys			
320	325	330	
Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu			
335	340	345	
Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp			
350	355	360	
Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln			
365	370	375	
Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser			
380	385	390	
Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu			
395	400	405	
Lys Arg Val Leu Leu Gly Pro			
410			

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacgggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 160  
gcccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
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gcggcgcttc ctgacgcage cgcagggtgt ggccgcgcgc gtgtgcttgg 150  
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tctcattcaa ag 1512

<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25				30	

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly
				35					40				45	

Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val
				50					55				60	

Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly
				65					70				75	

Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala
				80					85				90	

Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val
				95					100				105	

Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe
				110					115				120	

Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro
				125					130				135	

Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr
				140					145				150	

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu  
155 160 165  
Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn  
170 175 180  
Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr  
185 190 195  
Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln  
200 205 210  
Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr  
215 220

<210> 163  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 163  
tggtcttcgc cttgatcgta ttct 24

<210> 164  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 164  
gtgtactgag cggcggtag 20

<210> 165  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 165  
ctgaaggta tggctgccct cac 23

<210> 166  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
ccaggaggct catggaaag tcc 23

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
ccacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 168  
gagccaccta ccctgctccg aggccaggcc tgcagggcct catcgccag 50  
agggtgatca gtgagcagaa ggtatgcccgt ggccgaggcc ccccaggtgg 100  
ctggcgggca gggggacgga ggtatggcg aggaagcgga gccagagggg 150  
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<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp
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Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala
									25					30

Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val
									35					45

Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly
									50					60

Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val
									65					75

Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe
									80					90

Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg Ser Glu

95	100	105
Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser Thr		
110	115	120
Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly		
125	130	135
Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro		
140	145	150
Glu His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu		
155	160	165
Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val		
170	175	180
Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile		
185	190	195
Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu		
200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu Arg		
215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu		
230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr		
245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly		
260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg		
275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala		
290	295	300
Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val		
305	310	315
Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu Val Asn Leu		
320	325	330
Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser Thr Pro		
335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp His		
350	355	360
Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp		
365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln		

380                    385                    390

Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile  
395                    400                    405

Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly  
410                    415                    420

Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly  
425                    430                    435

Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro  
440                    445                    450

Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys  
455                    460                    465

Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys  
470                    475                    480

Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile  
485                    490                    495

Ser Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly  
500                    505                    510

Ser Asp Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe  
515                    520                    525

Thr Phe Gln Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro  
530                    535                    540

Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu  
545                    550                    555

His Cys Asp Cys Gly Leu Gln Gly Pro Ser Ser Arg Ile Val Gly  
560                    565                    570

Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu  
575                    580                    585

Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp  
590                    595                    600

Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met  
605                    610                    615

Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln  
620                    625                    630

Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu  
635                    640                    645

Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val  
650                    655                    660

Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val

	665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly			
680	685	690	
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly			
695	700	705	
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro			
710	715	720	
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg			
725	730	735	
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln			
740	745	750	
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg			
755	760	765	
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg			
770	775	780	
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser			
785	790	795	
Trp Ile Gln Gln Val Val Thr			
800			

<210> 170  
<211> 1327  
<212> DNA  
<213> Homo sapiens

<400> 170  
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atcctgcagc cctacgccga gaggatcccc gtggtgccca cggccgggat 100  
caccatcaac ttcacctccc agatctccct caccgggccc ggtgtcgaaa 150  
tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttccctc 200  
tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250  
ccccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300  
gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350  
cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
atgtggaca ttcaccctcc agtgtgagga ccggagctgc gtgaagaagc 450  
ccaacccgca gtgtgatggg cggcccgact gcagggacgg ctcggatgag 500  
gagcaactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550

agctgtgtcc tccgagggtg agtggccatg gcagggccagc ctccaggttc 600  
ggggtcgaca catctgtggg ggggcctca tcgctgaccg ctgggtgata 650  
acagctgccc actgcttcca ggaggacagc atggcctcca cggtgctgtg 700  
gaccgtgttc ctggcaagg tgtggcagaa ctcgcgctgg cctggagagg 750  
tgtccttcaa ggtgagccgc ctgctcctgc acccgtagca cgaagaggac 800  
agccatgact acgacgtggc gctgctgcag ctcgaccacc cggtggtgcg 850  
ctcggccgccc gtgcgcggc tctgcctgcc cgccgcgtcc cacttcttcg 900  
agccccggcct gcactgctgg attacgggct ggggcgcctt ggcgcagggc 950  
ggccccatca gcaacgtct gcagaaagtg gatgtgcagt tgatcccaca 1000  
ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcatgctgt 1050  
gtgccggcta ccgcaaggc aagaaggatg cctgtcaggg tgactcaggt 1100  
ggtcgcgtgg tgtgcaaggc actcagtggc cgctggttcc tggcggggct 1150  
ggtcagctgg ggcctggct gtggccggcc taactacttc ggcgtctaca 1200  
cccgcatcac aggtgtgatc agctggatcc agcaagtggt gacctgagga 1250  
actgcccccc tgcaaagcag ggcccaccc tcggactcag agagcccagg 1300  
gcaactgcca agcagggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccactgcttc cagg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173  
atggcctcca cgggtgtg gaccgtgtc ctggcaagg tgtggcagaa 50

<210> 174

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174  
tgccatgcg ctgaggaggc agaag 25

<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175  
aggcagggac acagagtcca ttcac 25

<210> 176

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176  
agtatgatt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177  
ggacgagggc agatctcggtt ctggggcaag ccgttgacac tcgctccctg 50  
ccaccgcccc ggctccgtgc cgccaaaggtt tcattttcca ctttctctgc 100  
ctccagtcggcc ccagccccgt gcggagagaaa gggctttacc ggccgggatt 150  
gctggaaaca ccaagagggtg gttttgtt tttaaaactt ctgtttcttg 200  
ggagggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250

tctggagcct ctgctattgc tttgctgcgg ggagccccgt accttttgt 300  
ccagaggac ggctggaaga taagctccac aaacccaaag ctacacagac 350  
tgaggtcaaa ccatctgtga ggtttaacct ccgcacctcc aaggaccag 400  
agcatgaagg atgctacctc tccgtcgccc acagccagcc cttagaagac 450  
tgcagttca acatgacagc taaaaccttt ttcatcattc acggatggac 500  
gatgagcggt atcttgaaa actggctgca caaactcgtg tcagccctgc 550  
acacaagaga gaaagacgcc aatgttagttg tggttgactg gctccccctg 600  
gccaccaggc tttacacgga tgcggtaat aataccaggg tggtggaca 650  
cagcattgcc aggatgctcg actggctgca ggagaaggac gattttctc 700  
tcggaatgt ccacttgatc ggctacagcc tcggagcgca cgtggccggg 750  
tatgcaggca acttcgtgaa aggaacggtg ggccgaatca caggtttgga 800  
tcctgcccggg cccatgtttg aaggggccga catccacaag aggctctc 850  
cgacgatgc agattttgtg gatgtcctcc acacctacac gcgttccttc 900  
gcttgagca ttggattca gatgcctgtg ggccacattt acatctaccc 950  
caatgggggt gacttccagc caggctgtgg actcaacgat gtcttggat 1000  
caattgcata tggaaacaatc acagaggtgg taaaatgtga gcatgagcga 1050  
gccgtccacc tctttgtga ctctctggtg aatcaggaca agccgagttt 1100  
tgccttccag tgcactgact ccaatcgctt caaaaagggg atctgtctga 1150  
gctgccgcaa gaaccgttgt aatagcattt gctacaatgc caagaaaatg 1200  
aggaacaaga ggaacagcaa aatgtaccta aaaacccggg caggcatgcc 1250  
tttcagaggt aacccctagt ccctggagtg tccctgagga aggcccttaa 1300  
taccccttc ttaataccat gctgcagagc agggcacatc ctagcccagg 1350  
agaagtggcc agcacaatcc aatcaaatcg ttgcaaatca gattacactg 1400  
tgcatgtcct aggaaaggga atctttacaa aataaacagt gtggaccct 1450  
aataaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa 1510

<210> 178  
<211> 354  
<212> PRT  
<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr
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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20				25						30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
					35			40						45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50				55						60
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65				70						75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80				85						90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95				100						105
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
					110			115						120
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125				130						135
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140				145						150
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155				160						165
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170				175						180
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185				190						195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200				205						210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215				220						225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230				235						240
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245				250						255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260				265						270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275				280						285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser  
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg  
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg  
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg  
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro  
350

<210> 179  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 179  
gtgagcatga gcgagccgtc cac 23

<210> 180  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 180  
gctattacaa cggttttgc ggcagc 26

<210> 181  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 181  
ttgactctt ggtaatcag gacaagccga gttttgcctt ccag 44

<210> 182  
<211> 3240  
<212> DNA  
<213> Homo sapiens

<400> 182  
cgacgcgtg ggccggacgcg tgggcctggg caaggccgg ggccgcgggc 50

cgagccacct cttccccctcc cccgcttccc tgtcgcgctc cgctggctgg 100  
acgcgctgga ggagtggagc agcacccggc cggccctggg ggctgacagt 150  
cgcaaaggtt tggcccaag aggaagtggt ctcaaaccggc ggcaggtggc 200  
gaccaggcca gaccaggggc gctcgctgcc tgcccgggg ctgttaggcga 250  
ggcgccgccc cagtgccgag accccggggct tcaggagccg gccccgggag 300  
agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcggaaagg 350  
caccggccct actcccgggc tgccgccc tcccgcccc cagccctggc 400  
atccagagta cgggtcgagc ccggggccatg gagccccct ggggaggcgg 450  
caccagggag cctggcgcc cggggctccg ccgcgacccccc atcgggtaga 500  
ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550  
gttggccacc ctccctctcc tcctccttgg aggccgtctg gcccatccag 600  
accggattat tttccaaat catgcttggt aggacccccc agcagtgctc 650  
ttagaagtgc agggcacctt acagaggccc ctggtccggg acagccgcac 700  
ctccctgcc aactgcacct ggctcatctt gggcagcaag gaacagactg 750  
tcaccatcag gttccagaag ctacacctgg cctgtggctc agagcgctta 800  
accctacgct cccctctcca gccactgatc tccctgtgtg aggcacccctcc 850  
cagccctctg cagctgccccg gggcaacgt caccatcaact tacagctatg 900  
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cctgccattt gctgctggac ccccatgtg gccggcggt ggccgtgcgc 1250  
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ccctggggccc cctgagagct cccgactact gcgtgtctc acccacttca 1350  
gcaatggcaa ggctgtcaact gtggagacac tgtctggcca ggctgttg 1400  
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ctggcctggg agctggcgaa ggcctaggtg agcgctgcta cagtgaggca 1550  
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caggaccaac cggagcccc cctggacccc acacagcagt cctggccctg 2600  
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gccccatggcca gacacccca g tcccttcacc accacctgct ccccacgcca 2950  
ccaccatttgc ggtggctgtt tttaaaaagt aaagttctta gaggatcata 3000  
ggtctggaca ctccatcctt gccaaacctc tacccaaaag tggccttaag 3050  
caccggaatg ccaattaact agagaccctc cagccccaa ggggaggatt 3100  
tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150  
ctcacaaaaa gagtgcaaca aatgcttcta ttccatagct acggcattgc 3200  
tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Gly Gly Ala Leu  
1 5 10 15

Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp  
20 25 . 30

Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro  
35 40 45

Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu  
50 55 60

Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys  
65 70 75

Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro  
80 85 90

Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu  
95 100 105

Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly  
110 115 120

Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln  
125 130 135

Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His  
140 145 150

Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys  
155 160 165

Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro  
170 175 180

Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr

▼

	185	190	195
Leu Glu Asp Phe Tyr Gly Val Phe Ser Sér Pro Gly Tyr Thr His			
200	205	210	
Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp			
215	220	225	
Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp			
230	235	240	
Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro			
245	250	255	
Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn			
260	265	270	
Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val			
275	280	285	
Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala			
290	295	300	
Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys			
305	310	315	
Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg			
320	325	330	
Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala			
335	340	345	
Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His			
350	355	360	
Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr			
365	370	375	
Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly			
380	385	390	
Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg			
395	400	405	
Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly			
410	415	420	
Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr			
425	430	435	
Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu			
440	445	450	
Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys			
455	460	465	
Leu Tyr Ala Ile Arg Thr Gln Glu Tyr Ser Ile Phe Ala Pro Leu			

470                  475                  480

Ser Arg Met Glu Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser  
485                  490                  495

Tyr Gly Gln Leu Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp  
500                  505                  510

Phe Pro Thr Glu Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu  
515                  520                  525

Arg Ser Leu Leu Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly  
530                  535                  540

Gly Pro Gly Ala Arg Arg Gln Arg Gly Arg Leu Met Arg Arg  
545                  550                  555

Leu Val Arg Arg Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn  
560                  565                  570

Thr Pro Ala Arg Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser  
575                  580                  585

Ala Ala Pro Leu Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg  
590                  595                  600

Glu Gly Gly Ala Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro  
605                  610                  615

Leu Pro Ile Lys Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala  
620                  625                  630

Pro Thr Thr Val Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro  
635                  640                  645

Leu Glu Pro Ser Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly  
650                  655                  660

Arg Leu Leu Pro Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro  
665                  670                  675

Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp  
680                  685                  690

Val Leu Leu Val Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu  
695                  700                  705

Ala Glu Asp Glu Pro Leu Leu Thr  
710

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tgcctgctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgcctggga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
cgagctgggc gagaagtagg ggagggcggt gctccgcccgc ggtggcggtt 50

gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgcgtc ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150  
aataaaaacat cgccccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
tgcggtggc actaactgtg acatctatga cctttttat catgcacaa 250  
gccctgaac catatatgt tatcaactgga tttgaagtca ccgttatctt 300  
attttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350  
tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400  
atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450  
agttggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500  
acggggccct tatttaccgg aagttctgt tcaatccag cggtccttac 550  
cagaaaaaagc ctgtgcatga aaaaaaaagaa gtttgtaat tttatattac 600  
tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650  
aaaaaaaaaaa aaa 663

<210> 190  
<211> 152  
<212> PRT  
<213> Homo sapiens

<400> 190  
Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe  
1 5 10 15  
  
Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val  
20 25 30  
  
Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr  
35 40 45  
  
Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile  
50 55 60  
  
Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe  
65 70 75  
  
Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe  
80 85 90  
  
Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr  
95 100 105  
  
Leu Thr Val Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys  
110 115 120  
  
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn  
125 130 135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
140 145 150

Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

<400> 191  
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50  
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaaagtg 100  
ctgctgctgg gtctgcagac gcgtatggata acgtgcagcc gaaaataaaa 150  
catcgccccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
ggcactaact gngacatcta tgacctttt tatnatcgca caagccccctg 250  
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atactttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
gcctttgctt gatattatca actcactggt aacaacagta ttcatgctca 400  
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttgg 450  
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cgttttgcag aacctactca ggcag 25

<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193  
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 194  
aaagtgcgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195  
<211> 1879  
<212> DNA  
<213> Homo sapien

<400> 195  
cagccccgcg cgccggccga gtcgctgagc cgcggtgcc ggacgggacg 50  
ggaccggcta ggctgggcgc gccccccggg ccccgccgtg ggcattggcg 100  
caactggcccg ggcgtgctg ctgcctctgc tggcccaagt gtcctgcgc 150  
gccgccccgg agctggccccc cgccgccttc acgctgcccc tccgggtggc 200  
cgcgccacg aaccgcgtag ttgcgcaccc cccgggaccc gggacccctg 250  
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aaataattaa aaaaaaaact tcattctaa 1879

<210> 196  
<211> 518  
<212> PRT  
<213> Homo sapien

<400> 196  
Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln  
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Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr  
20 25 30  
  
Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro  
35 40 45  
  
Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu  
50 55 60

Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala  
65 70 75

Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg  
80 85 90

Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu  
95 100 105

Gln Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Ala Gly  
110 115 120

Thr Pro His Ser Tyr Ile Asp Thr Tyr Phe Asp Thr Glu Arg Ser  
125 130 135

Ser Thr Tyr Arg Ser Lys Gly Phe Asp Val Thr Val Lys Tyr Thr  
140 145 150

Gln Gly Ser Trp Thr Gly Phe Val Gly Glu Asp Leu Val Thr Ile  
155 160 165

Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn Ile Ala Thr Ile  
170 175 180

Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys Trp Asn Gly  
185 190 195

Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser Ser Ser  
200 205 210

Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile Pro  
215 220 225

Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala  
230 235 240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu  
245 250 255

Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu  
260 265 270

Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly  
275 280 285

Gln Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala  
290 295 300

Ile Val Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val  
305 310 315

Phe Asp Ala Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro  
320 325 330

Glu Phe Ser Asp Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp  
335 340 345

Thr Asn Ser Glu Thr Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile  
350 355 360

Tyr Leu Arg Asp Glu Asn Ser Ser Arg Ser Phe Arg Ile Thr Ile  
365 370 375

Leu Pro Gln Leu Tyr Ile Gln Pro Met Met Gly Ala Gly Leu Asn  
380 385 390

Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro Ser Thr Asn Ala Leu  
395 400 405

Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp  
410 415 420

Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu  
425 430 435

Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr  
440 445 450

Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu  
455 460 465

Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly  
470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg  
485 490 495

Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser  
500 505 510 .

Ser Leu Val Arg His Arg Trp Lys  
515

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgcagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaatttggta ggccaaagc 19

<210> 199  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 199  
ggatgtagcc agcaactgtg 20

<210> 200  
<211> 19  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 200  
gccttggctc gttctcttc 19

<210> 201  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 201  
ggtcctgtgc ctggatgg 18

<210> 202  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 202  
gacaagacta cctccgttgg tc 22

<210> 203  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 203  
tgatgcacag ttcagcacct gttg 24

<210> 204

<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 204  
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
<211> 1939  
<212> DNA  
<213> Homo sapiens

<400> 205  
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taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
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Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
									35		40			45

Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
									50		55			60

Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
									65		70			75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile  
80 85 90

Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe  
95 100 105

Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile  
110 115 120

His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe  
125 130 135

Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr  
140 145 150

His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val  
155 160 165

Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe  
170 175 180

Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg  
185 190 195

Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu  
200 205 210

Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala  
215 220 225

His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro  
230 235 240

Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu  
245 250 255

Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu  
260 265 270

Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys  
275 280 285

His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala  
290 295 300

His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro  
305 310 315

Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser  
320 325 330

Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr  
335 340 345

Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser  
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Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln  
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Leu Ser

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 207

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<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagttgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 209

ctttctgagc tctgagccac gggtggacat cctcatccac aatgc 45

<210> 210

<211> 3716

<212> DNA

<213> Homo sapiens

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caagcctcag gccagccacc tcccaccatc cgctggttgc tgaatggca 200

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<210> 211  
<211> 985  
<212> PRT  
<213> Homo sapiens

<400> 211  
Met Gly Gly Met Ala Gln Asp Ser Pro Pro Gln Ile Leu Val His  
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Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro Ala Arg Met Ser  
20 25 30  
Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu  
35 40 45  
Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu  
50 55 60  
Leu Pro Asp Gly Thr Leu Leu Leu Gln Pro Pro Ala Arg Gly  
65 70 75  
His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr  
80 85 90  
Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly  
95 100 105  
Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln  
110 115 120  
Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu  
125 130 135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp  
140 145 150

Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val  
155 160 165

Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu  
170 175 180

Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu  
185 190 195

Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr  
200 205 210

Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val  
215 220 225

Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro  
230 235 240

Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala  
245 250 255

Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly  
260 265 270

Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser  
275 280 285

Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys  
290 295 300

Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val  
305 310 315

Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln  
320 325 330

Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp  
335 340 345

Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr  
350 355 360

Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp  
365 370 375

Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met  
380 385 390

Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly  
395 400 405

Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala  
410 415 420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr  
425 430 435

Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala  
440 445 450

Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Gly Thr Ala Val  
455 460 465

Cys Ile His Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly  
470 475 480

Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met  
485 490 495

Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr  
500 505 510

Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg  
515 520 525

Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu  
530 535 540

Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp  
545 550 555

Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser  
560 565 570

Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu  
575 580 585

Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp  
590 595 600

Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu  
605 610 615

Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln  
620 625 630

His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu  
635 640 645

Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser  
650 655 660

Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala  
665 670 675

Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg  
680 685 690

His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr  
695 700 705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser  
710 715 720

Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys  
725 730 735

Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro  
740 745 750

Ala Ser Ser Arg Leu Ser Ser Ser Leu Ser Ser Leu Gly Glu  
755 760 765

Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu  
770 775 780

Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro  
785 790 795

Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser  
800 805 810

Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly  
815 820 825

Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro  
830 835 840

Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp  
845 850 855

Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu  
860 865 870

Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala  
875 880 885

Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu  
890 895 900

Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro  
905 910 915

Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro  
920 925 930

Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser  
935 940 945

His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp  
950 955 960

Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro  
965 970 975

Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser  
980 985

<210> 212  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 212  
gaagggacct acatgtgtgt ggcc 24

<210> 213  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 213  
actgacccttc cagctgagcc acac 24

<210> 214  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 214  
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215  
<211> 2749  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1869, 1887  
<223> unknown base

<400> 215  
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gcgggttcga agggacact gtgtccctgc agtgcaccta cagggaaagag 150  
ctgagggacc accggaagta ctggtgcaagg aagggtggga tcctttctc 200  
tcgctgtct ggcaccatct atgcagaaga agaaggccag gagacaatga 250  
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accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggt 350  
cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400  
caggaccctg ctgtcctccc tccccttctc ccaccccca gcctctggct 450  
acaacacgcc tgcaaaaaaa ggcaaaaagct cagcaaaccc agcccccagg 500  
attgacttct cctgggctct accccggcagc caccacagcc aagcagggga 550  
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gacctttta taaataaaaat gttcatcagc tgcataaaaaa aaaaaaaaaa 2749

<210> 216  
<211> 332  
<212> PRT  
<213> Homo sapiens

<400> 216  
Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly  
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Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly  
20 25 30

Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp  
35 40 45

His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg

	50	55	60
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Gly Gln Glu Thr Met			
65	70	75	
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu			
80	85	90	
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr			
95	100	105	
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile			
110	115	120	
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser			
125	130	135	
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala			
140	145	150	
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu			
155	160	165	
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu			
170	175	180	
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr			
185	190	195	
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro			
200	205	210	
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala			
215	220	225	
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg			
230	235	240	
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu			
245	250	255	
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His			
260	265	270	
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln			
275	280	285	
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys			
290	295	300	
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro			
305	310	315	
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val			
320	325	330	
Ser Ala			

<210> 217  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 217  
ccctgcagtg cacctacagg gaag 24

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 218  
ctgtcttccc ctgcttggct gtgg 24

<210> 219  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 219  
ggtgtggatac ctcttctctc gctgctctgg ccacatc 47

<210> 220  
<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 220  
tttgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50  
ggggtgtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100  
cagtgtgaaa gaaccagtgg tctcgctctg ttgcccaaggc tagagtgtac 150  
tggcgtgatc atagctcaact gcagcctcag actcctggac ttgagaaatc 200  
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cctgtttctt ctccttctgt gagtggacca cggaggctgg tgagctgcct 300  
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ccggccggcat agaaggccagg agcaggggctc tcagaaggcg gtggtgccca 400

gctgggatca tgggttggc cctggctgt ctgctcagct gcctgctacc 450  
ctccagttag gccaagctct acggtcgtt tgaactggcc agagtgtac 500  
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gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900  
cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
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Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20				25					30	

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35				40					45	

Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50				55					60	

Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65				70					75	

Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80				85					90	

Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95				100					105	

Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110				115					120	

Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125				130					135	

Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe
				140				145		

<210> 222  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 222  
gggatcatgt tgttgccct ggtc 24

<210> 223  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 223  
gcaaggcaga cccagtcagc cag 23

<210> 224  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 224  
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225  
<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
agccgctgcc ccggggccggg cgccccgcggc ggcaccatga gtcccccgtc 50  
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cgagcaactg gctgtacctg gccaaagctgt cgtcggtgaaa gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200  
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gctgtgcctt tgcagtcatg cccgagtcac ct当地cacagc gctgttcctc 1900  
catgaaactg aaaaacacac acacacacac acacacacac 1950  
acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000  
ctgtgcctt gcagtcatgc cc当地gtcacc tt当地cacagca ct当地tcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe  
1 5 10 15

Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys  
20 25 30

Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys  
35 40 45

Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
50 55 60

Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
65 70 75

Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
80 85 90

Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
95 100 105

Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
110 115 120

Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys  
125 130 135

Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe  
140 145 150

Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe  
155 160 165

Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser  
170 175 180

Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg  
185 190 195

Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly  
200 205 210

Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro

215 220 225

Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly  
230 235 240

Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu  
245 250 255

Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu  
260 265 270

Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg  
275 280 285

Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser  
290 295 300

Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe  
305 310 315

His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe  
320 325 330

His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val  
335 340 345

Glu Leu His Thr Cys Arg  
350

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtgggaga ctgtttaaat tatcggcc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgcggca gtgccagcgg ctcgtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggacgcgtg ggcggacgcg tggcgacg cgtggcgga cgcgtggct 50

gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcgca 100

gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150

aggagacccc tcttcttggc cctggctgtc ctggcacca cagtcctttg 200

ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250

cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300

cgccgcgtgg gtgcctgaa ggaggaggc ggagactgcc acagctgctg 350

ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttgggagg 400

cgcaggcgaa gctgatggag caggagacg ccctgcggga actgcgtgag 450

cgcgtgaccc agggcttggc tgaagccggc agggccgtg aggacgtccg 500

cactgagctg ttccgggcgc tggaggccgt gaggctccag aacaactcct 550

gcgagccgtg ccccacgtcg tggctgtcct tcgagggctc ctgctacttt 600

ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650

tgccagcgcg cacctggta tcgttgggg cctggatgag cagggcttcc 700

tcactcgaaa cacgcgtggc cgtggtaact ggctggccct gagggctgtg 750

cgcacatctgg gcaagggttca gggctaccag tgggtggacg gagtctctct 800

cagttcagc cactggaacc agggagagcc caatgacgct tggggcgcg 850

agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900

gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950

ccgcccagtg ccctggagcc gcgcacattg cagcatgtcg tatcctgggg 1000

gctgctcacc tccctggctc ctggagctga ttgccaaaga gttttttct 1050

tcctcatcca cgcgtgtca gtctcagaaa cacttggccc aacatagccc 1100

tgtccagccc agtgcctggg ctctggacc tccatgccga cctcatccta 1150

actccactca cgcatccccca acctaaccctc cactagctcc aaaatccctg 1200  
ctccctgcgtc cccgtgatat gcctccactt ctctccctaa ccaaggtag 1250  
gtgactgagg actggagctg tttgggtttc tcgcatttc caccaaactg 1300  
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
aaaaaa 1355

<210> 231  
<211> 293  
<212> PRT  
<213> Homo sapiens

<400> 231  
Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu  
1 5 10 15  
Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
20 25 30  
Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
35 40 45  
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
50 55 60  
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
65 70 75  
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
80 85 90  
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
95 100 105  
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
110 115 120  
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
125 130 135  
Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg  
140 145 150  
Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys  
155 160 165  
Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser  
170 175 180  
Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp  
185 190 195  
Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly  
200 205 210

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu  
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val  
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro  
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr  
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp  
275 280 285

Ile Cys Glu Lys Arg His Asn Cys  
290

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gagggtgatc cgaccgggg aaggtcgctg ggcagggcga 50  
gttggaaag cggcagcccc cgccgcccc gcagcccctt ctccctcctt 100  
ctccccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150  
agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200  
gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgcccggccg 250  
cgctcccgct gtcctgccc ggtgatggaa aaccccagcc cggccgcccgc 300  
cctggcaag gccctctgcg ctctcctcct ggccactctc ggcggccggc 350  
gccagcctct tgaaaaatggag tccatctgtt ccggcagagc cccggccaaa 400  
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ggtgaccgag ataacgtcct cctctccag ccacccggcc aactccttct 950  
actaccccgcg gctgaaggcc ctgcctccca tcgcccagggt gacactgctg 1000  
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agcgggggccc acttgagaag tgaataaatg gggcggttgc ggaagcgtca 1750  
gtgttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800  
tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys
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Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly
					20				25				30	
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
					35				40				45	
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
					50				55				60	
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
					65				70				75	
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
					80				85				90	
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
					95				100				105	
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Gln	Ser	Val	
					110				115				120	
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln
					125				130				135	
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser
					140				145				150	
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val
					155				160				165	

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala  
170 175 180

Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe  
185 190 195

Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val  
200 205 210

Thr Glu Ile Thr Ser Ser Pro Ser His Pro Ala Asn Ser Phe  
215 220 225

Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr  
230 235 240

Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala  
245 250 255

Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser  
260 265 270

Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser  
275 280 285

Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser  
290 295 300

Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro  
305 310 315

Cys Pro Glu Leu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys  
320 325 330

Val

<210> 237  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 237  
cagcactgcc agggaaagag gg 22

<210> 238  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 238  
caggactcgc tacgtccg 18

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 239  
cagccccttc tcctcccttc tccc 24

<210> 240  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 240  
gcagtttatca gggacgcact cagcc 25

<210> 241  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 241  
ccagcgagag gcagatag 18

<210> 242  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 242  
cggtcaccgt gtcctgcggg atg 23

<210> 243  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
cagccccttc tcctcccttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894  
<212> DNA  
<213> Homo sapiens

<400> 244  
ggcggcggtcc gtgagggct cctttggca gggtagtgtt ttgggtgtccc 50  
tgtcttcgtt gatattgaca aactgaagct ttccctgcacc actggactta 100  
aggaagagtgt tactcgtagg cgacagctt tagtgccgg ccggccgctc 150  
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
tctacatcca ggagcctccc acgaatggaa aggttttatt gaaaactaca 250  
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagctt 300  
cagaaatttt atccaacttt gtttggaaagc ttattatgac aataccattt 350  
ttcatagagt tgtgcctggt ttcatagtc aaggcggaga tcctactggc 400  
acagggagtg gtggagagtc tatctatgga gcgcattca aagatgaatt 450  
tcattcacgg ttgcgttta atcggagagg actgggtgcc atggcaaatg 500  
ctggttctca tgataatggc agccagttt tcttcacact gggtcgagca 550  
gatgaactta acaataagca taccatcttt ggaaaggta cagggatac 600  
agtatataaac atgttgcgac tgtcagaagt agacattgtat gatgacgaaa 650  
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tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750  
agaggaggaa gtaaagaaat tgaaacccaa aggacacaaaa aatttttagtt 800  
tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaatcga 850  
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ggatgatcca catctcagtt ctgttccagt tgtagaaagt gaaaaagggtg 950  
atgcaccaga ttttagttgat gatggagaag atgaaagtgc agagcatgtat 1000  
gaatatattt atgggtatgaa aaagaacctg atgagagaaa gaattgcca 1050  
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tcacatgtac ttcatgttga ggataaaagc agaaaaagtga aagatgcaag 1500  
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ataaaagaag gagggaaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600  
agaagataaa atgagaataa tgataaccag aacttgctgg aatgtgcct 1650  
acaatggcct tgtaacagcc attgttccca acagcatcac tttagggtgt 1700  
gaaaagaagt attttgaac ctgttgcctg gtttgaaaa acaattatct 1750  
tgtttgcaa attgtgaaat gatgtaaagca aatgttttg gttactggta 1800  
catgtgtttt ttccttagctg acctttata ttgctaaatc taaaataaaa 1850  
taacttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

Met	Ser	Asn	Ile	Tyr	Ile	Gln	Glu	Pro	Pro	Thr	Asn	Gly	Lys	Val
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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
					20				25					30

Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
				35				40						45

Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
				50				55						60

Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
			65					70						75

Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
					80			85						90

Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
				95				100						105

Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala
					110			115						120

Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly
				125				130						135

Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp  
140 145 150

Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu  
155 160 165

Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys  
170 175 180

Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys  
185 190 195

Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu  
200 205 210

Ala Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met  
215 220 225

Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro  
230 235 240

His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala  
245 250 255

Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp  
260 265 270

Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile  
275 280 285

Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala  
290 295 300

Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu  
305 310 315

Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala  
320 325 330

Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg  
335 340 345

Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr  
350 355 360

Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser  
365 370 375

Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn  
380 385 390

Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu  
395 400 405

Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met  
410 415 420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp  
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg  
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met  
455 460 465

Arg Glu Lys Lys Glu Arg Arg  
470

<210> 246  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 246  
tgcggagatc ctactggcac aggg 24

<210> 247  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 247  
cgagtttagtc agagcatg 18

<210> 248  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 248  
cagatggtgtc tgttgccg 18

<210> 249  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 249  
caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 250  
ctggttcagc agtgcaaggg tctg 24

<210> 251  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
cctctccgat taaaacgc 18

<210> 252  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 252  
gagaggactg gttgccatgg caaatgctgg ttctcatgtat aatgg 45

<210> 253  
<211> 2456  
<212> DNA  
<213> Homo sapiens

<400> 253  
cgccgcgtt gggctggaa gttccgcaca ggtccgtgcc gggcgagaga 50  
gatgctgcccgccccc ggccgcctc ggcttgagg cgagagaagt gtcccagacc 100  
catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150  
ttctccttcg ggtccggac tctggctcc accaccgtgg ccggccggcgg 200  
gaccagcaca ggcggcgaaa tctccttcgg aacggaaacg tctagcaacc 250  
cttctgtggg gctcaatttt gaaatcttg gaagtaatcc aactccagca 300  
actacatctg ctcctcaag tggtttgaa accgggctct ttggatctaa 350  
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ccaagaggcc tcaagtggtc accaaatatg gaaccctgca aggaaaacag 450  
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aaaaaaa 2456

<210> 254

<211> 545

<212> PRT

<213> Homo sapiens

<400> 254

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Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly  
35 40 45

Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser  
50 55 60

Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly  
65 70 75

Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg  
80 85 90

Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met  
95 100 105

His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe  
110 115 120

Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro  
125 130 135

Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro  
140 145 150

Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg  
155 160 165

Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu  
170 175 180

Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu  
185 190 195

Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg  
200 205 210

Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val  
215 220 225

Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met  
230 235 240

Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser  
245 250 255

Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val  
260 265 270

Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp  
275 280 285

Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala  
290 295 300

Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp  
305 310 315

Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser  
320 325 330

Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His  
335 340 345

Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile  
350 355 360

Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala  
365 370 375

Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg  
380 385 390

Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg  
395 400 405

Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp  
410 415 420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro  
425 430 435

Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu  
440 445 450

Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn  
455 460 465

Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp  
470 475 480

Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met  
485 490 495

Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr  
500 505 510

Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala  
515 520 525

Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu  
530 535 540

Pro Gln Glu Trp Ala  
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<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

aggtgcctgc aggagtcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257  
gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45  
  
<210> 258  
<211> 2764  
<212> DNA  
<213> Homo sapiens  
  
<400> 258  
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ggagattctg gatacgagtg caggagtca gatggtgcc ggagggctg 150  
tgcacatctcg tgccctgctc tttctcctac ccccgacaag actggacagg 200  
gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250  
agggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300  
acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350  
cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttcttc 400  
gggtggagag aggaagctat gtgacatata attcatgaa cgatgggttc 450  
tttctaaaag taacagtgct cagttcacg cccagaccc aggaccacaa 500  
caccgaccc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550  
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ccagagaacc tgagagtgat gtttcccaa gcaaacagga cagtcctgga 950  
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tcaccttaaa aaaa 2764

<210> 259  
<211> 544  
<212> PRT  
<213> Homo sapiens

<400> 259  
Met Leu Leu Pro Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln  
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Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met  
20 25 30  
Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr  
35 40 45  
Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp  
50 55 60  
Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr  
65 70 75  
Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe  
80 85 90  
Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile  
95 100 105  
Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val  
110 115 120  
Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe  
125 130 135  
Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp  
140 145 150  
His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly  
155 160 165  
Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro  
170 175 180  
Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu  
185 190 195  
Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys  
200 205 210  
Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro  
215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser  
230 235 240

His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val  
245 250 255

Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg  
260 265 270

Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro  
275 280 285

Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val  
290 295 300

Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly  
305 310 315

Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala  
320 325 330

Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln  
335 340 345

Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu  
350 355 360

His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser  
365 370 375

Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu  
380 385 390

Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile  
395 400 405

Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile  
410 415 420

Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe  
425 430 435

Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr  
440 445 450

Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn  
455 460 465

Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser  
470 475 480

Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu  
485 490 495

Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu  
500 505 510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg  
515 520 525  
Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu  
530 535 540  
Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaaggctgc gcctggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagagggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

ggagctgcc caattcaaa tggagcacga aggagatgc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263 .

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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttgag 100

caacagaaaa ctctcaaaca aagaaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtgaaac caatttttt taccagagga 200

aatgaatacg actagtcatc acatcgccca gctaagatct gathtagaca 250  
atggaaacaa ttcttccag tacaagctt tgggagctgg agctggaagt 300  
acttttatca ttgatgaaag aacaggtgac atatatgccca tacagaagct 350  
tgatagagag gagcgatccc tctacatctt aagagccag gtaatagaca 400  
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tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500  
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550  
caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600  
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taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750  
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agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400  
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cagactatca gtgcagtggta tagagatgaa tccatagaag agcaccattt 1550  
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gaaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950  
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aaaccacaag cgctgagatc aggacccat acaggcagtc tttgcaagtt 2100  
ggccccgaca gtgcattatt cagaaattc attctggaaa agctcgaaga 2150  
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atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800  
tatagtcaga gaaatTTCA tgaattattc catgaagtat tgTTTcctt 2850  
atTTaaa 2857

<210> 264  
<211> 772  
<212> PRT  
<213> Homo sapiens

<400> 264

Met Asn Cys Tyr Leu Leu Leu Arg Phe Met Leu Gly Ile Pro Leu  
1 5 10 15

Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys  
20 25 30

Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp  
35 40 45

Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser  
50 55 60

His His Ile Gly Gln Leu Arg Ser Asp Leu Asp Asn Gly Asn Asn  
65 70 75

Ser Phe Gln Tyr Lys Leu Leu Gly Ala Gly Ala Gly Ser Thr Phe  
80 85 90

Ile Ile Asp Glu Arg Thr Gly Asp Ile Tyr Ala Ile Gln Lys Leu  
95 100 105

Asp Arg Glu Glu Arg Ser Leu Tyr Ile Leu Arg Ala Gln Val Ile  
110 115 120

Asp Ile Ala Thr Gly Arg Ala Val Glu Pro Glu Ser Glu Phe Val  
125 130 135

Ile Lys Val Ser Asp Ile Asn Asp Asn Glu Pro Lys Phe Leu Asp  
140 145 150

Glu Pro Tyr Glu Ala Ile Val Pro Glu Met Ser Pro Glu Gly Thr  
155 160 165

Leu Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Ser Ser  
170 175 180

Gly Asn Asn Ala Arg Leu Leu Tyr Ser Leu Leu Gln Gly Gln Pro  
185 190 195

Tyr Phe Ser Val Glu Pro Thr Thr Gly Val Ile Arg Ile Ser Ser  
200 205 210

Lys Met Asp Arg Glu Leu Gln Asp Glu Tyr Trp Val Ile Ile Gln  
215 220 225

Ala Lys Asp Met Ile Gly Gln Pro Gly Ala Leu Ser Gly Thr Thr  
230 235 240

Ser Val Leu Ile Lys Leu Ser Asp Val Asn Asp Asn Lys Pro Ile  
245 250 255

Phe Lys Glu Ser Leu Tyr Arg Leu Thr Val Ser Glu Ser Ala Pro  
260 265 270

Thr Gly Thr Ser Ile Gly Thr Ile Met Ala Tyr Asp Asn Asp Ile  
275 280 285

Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser  
290 295 300

Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile  
305 310 315

Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr  
320 325 330

Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu  
335 340 345

Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln  
350 355 360

Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr  
365 370 375

Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly  
380 385 390

Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg  
395 400 405

Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly  
410 415 420

Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp  
425 430 435

Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln  
440 445 450

Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp  
455 460 465

His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu  
470 475 480

Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp  
485 490 495

Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser  
500 505 510

Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln  
515 520 525

Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu  
530 535 540

Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn  
545 550 555

Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val  
560 565 570

Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln  
575 580 585

Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala  
590 595 600

Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr  
605 610 615

Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys  
620 625 630

Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly  
635 640 645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg  
650 655 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser  
665 670 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro  
680 685 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu  
695 700 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr  
710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser  
725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu  
740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly  
755 760 765

Ser Ala Val Gln Ser Asn Asn  
770

<210> 265  
<211> 349  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 24, 60, 141, 226, 228, 249, 252  
<223> unknown base

<400> 265  
atttcaaggc cagccatatt ttntgttga accaacaaca ggagtataa 50  
gaatattttn taaaatggat agagaactgc aagatgagta ttgggtatac 100

attcaagcca aggacatgat tggtcagcca ggagcggtgt ntggAACAC 150  
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200  
aagaaaAGTTT ataccgcttg actgtntntg aatctgcacc cactgggant 250  
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300  
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 266  
cttgactgtc tctgaatctg caccc 25

<210> 267  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 267  
aagtgggtgga agcctccagt gtgg 24

<210> 268  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400>.268  
ccactacggt attagagcaa aagttaaaaa ccacatggc tcctggagca 50  
gc 52

<210> 269  
<211> 2747  
<212> DNA  
<213> Homo sapiens

<400> 269  
gcaacacctag cttcttagtat ccagactcca ggcggcccc gggcgcgac 50  
cccaaccccg acccagagct tctccagcgg cggcgagcg agcagggctc 100  
cccgcccttaa ctccctccgc gggcccagc caccccggtt agtccgggtt 150

ccccacacctgc aaactctccg cttctgcac ctgccacccc tgagccagcg 200  
cggggccccc agcgagtcat ggccaacgcg gggctgcagc tggggctt 250  
cattctcgcc ttccctggat ggatcggcgc catcgtcagc actgccctgc 300  
cccagtgtag gatttactcc tatgcggcg acaacatcg taccggccag 350  
ccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccggca 400  
gatccagtgc aaagtctttg actccttgcgtaatctgagc agcacattgc 450  
aagcaacccg tgcccttgatg gtgggtggca tcctcctgg agtgatagca 500  
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tgaggtgcag aagatgagga tggctgtcat tgggggtgcg atatttc 600  
ttgcaggcttgc ggctattttt gttgccacag catggtatgg caatagaatc 650  
gttcaagaat tctatgaccc tatgacccca gtcaatgcca ggtacgaatt 700  
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gaggtgcctt actttgcgt tcctgtcccc gaaaaacaac ctcttacccca 800  
acaccaaggc cctatccaaa acctgcaccc tccagcggga aagactacgt 850  
gtgacacaga gcaaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900  
acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950  
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gttaaaatac tcagtgctaa acatggctt atcttatttt atcttcttc 1050  
ctcaatatac gagggaaat tttccattt gtattactgc ttcccatgaa 1100  
gtaatcatac tcaaattgggg gaagggtgc tccttaata tatatagata 1150  
tgttatatac catgttttc tattaaaaat agacagtaaa atactattct 1200  
cattatgtt atactagcat actaaaaata tctctaaaat agttaatgt 1250  
atttaaattcc atattgatga agatgtttat tggtatattt tcttttcgt 1300  
ccttatatac atatgtaca gtcaaatac atttactctt cttcattagc 1350  
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ataatcttat agcacttgca tcgttattaa gcccttattt gttttgtgtt 1500  
tcattggtct ctatctcctg aatctaacad atttcatagc ctacattttt 1550  
gtttctaaq ccaqaqaqaa tttattacaa atcaqaactt tqqacqcaaa 1600

tctttctgca tgaccaaagt gataaaattcc tggacccctt cccacacaat 1650  
ccctgtactc tgaccatag cactcttggtt tgcttgaaa atatttgc 1700  
aatttagtag ctgcattgtg ttccccagg tggtaaca caactttatt 1750  
gattgaattt ttaagctact tattcatagt tttatatccc cctaaactac 1800  
ctttttgttc cccatttcctt aattgtattg ttttcccaag tgtaattatc 1850  
atgcgtttta tatcttccta ataaggtgtg gtctgttgt ctgaacaaag 1900  
tgcttagactt tctggagtga taatctggtg acaaataattc tctctgtac 1950  
tgtaagcaag tcacttaatc tttctacctc tttttctat ctgccaaatt 2000  
gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050  
tttatattac tcttattctt tgaacatgaa ctatgcctat gtagtgtctt 2100  
tatttgctca gctggctgag acactgaaga agtcaactgaa caaaacctac 2150  
acacgtacct tcattgtgatt cactgccttc ctctctctac cagtctattt 2200  
ccactgaaca aaacctacac acatacccttc atgtggttca gtgccttc 2250  
ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300  
gtggctcagt gccttcctct ctctaccagt ctattccat tcttcagct 2350  
gtgtctgaca tgtttgcgt ctgttccatt ttaacaactg ctcttacttt 2400  
tccagtctgt acagaatgct atttcacttg agcaagatga tgtaatggaa 2450  
agggtgttgg cactgggtgc tggagacctg gatttgagtc ttgggtctat 2500  
caatcaccgt ctgtgttga gcaaggcatt tggctgctgt aagcttattg 2550  
cttcattctgt aagcgggtgt ttgtaattcc tgatctccc acctcacagt 2600  
gatgttgggg ggatccagtg agatagaata catgtaagtg tggtttgta 2650  
ataaaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700  
gttttgggtgt tgctttcaa atgttgaaa ataaaaaaaaa tgttaag 2747

<210> 270  
<211> 211  
<212> PRT  
<213> Homo sapiens

<400> 270  
Met Ala Asn Ala Gly Leu Gln Leu Leu Gly Phe Ile Leu Ala Phe  
1 5 10 15  
Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

20	25	30
Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala		
35	40	45
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly		
50	55	60
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser		
65	70	75
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu		
80	85	90
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met		
95	100	105
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val		
110	115	120
Ile Gly Gly Ala Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val		
125	130	135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp		
140	145	150
Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu		
155	160	165
Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala		
170	175	180
Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr		
185	190	195
Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr		
200	205	210
Val		

<210> 271  
<211> 564  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 21, 69, 163, 434, 436, 444  
<223> unknown base

<400> 271  
ttctggccaa acccggggct ncagctgttg ggcttcatct cgccttcctg 50  
ggatggatcg ggcacatcnt cacactgccc ttccccagtg gaggattta 100  
ctcccttatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
cttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250  
tcatgggtt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300  
gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350  
gaggatggct gtcattgggg gcgcgatatt tcttcttgcg ggtctggcta 400  
tttagttgc cacagcatgg tatggcaata gaancntca acanttctat 450  
gaccctatga ccccagtcaa tgccaggtac gaatttggtc aggctcttt 500  
cactggctgg gctgctgctt ctctctgcct tctggaggt gccctacttt 550  
gctgttcctg tccc 564

<210> 272  
<211> 498  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341  
<223> unknown base

<400> 272  
acccttgacc caacgcggcc ccccgaccgn ttcatggcca aacgcgggn 50  
tccagctgtt gggcttcatt ctccccttcc tggatggac cgccgcggcat 100  
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150  
acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200  
tcgcagagca ccgggcagat ccagtgcaaa gtcttgact cccttgctga 250  
atctgagcag cacattgcaa gcaaccgtg cttgtatggat ggttggcatc 300  
ctcctggag ttagtgcatt cttnntggcc accgttgnn ntgaagtgt 350  
tgaagtgcatt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400  
gggggcgcga tattttctt tgcaggctg gctatttttag ttgccacagc 450  
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273  
<211> 552  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394  
<223> unknown base

<400> 273  
gggcccgacc attatccaac cgggntcaact gttggctcat ctccctcctg 50  
gatgaancgc gccatcntca gactccctgc cccatggaga tttncctat 100  
gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac ccntgccctg atggtggtt 250  
gcatcctcct gggagtgata gcaatcttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttggaaaga cgatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gcgatatttc ttcttgcagg tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcggtcaa gaattctatg accctatgac 450  
cccagtcaat gccaggtacg aatttggtca ggctctcttc actggctggg 500  
ctgctgcttc tctctgcctt ctgggaggtg ccctactttt ctgttcctgc 550  
ga 552

<210> 274  
<211> 526  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407  
<223> unknown base

<400> 274  
attctccct cctggatgga tcgcnccacc gtcacattgc cttccccan 50  
tggaggattt actcctatgc tggcgacaac atcgtgaccc cccaggccat 100  
ttaccgaggg gctttggatg tcntgcntgt cgccagacac cgggcagatc 150  
ccagtgcaaa gtcttgact cttgctgaa tctgagcagc acattgcaag 200  
caacccgtgc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
ttgtggccac cggtggcatg aagtgtatga agtgcttggaa agacgatgag 300  
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgg 350  
cagggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400  
cnngnnntct atgaccctat gaccccgatc aatgccaggt acgaatttgg 450

tcaggctctc ttcactggct gggctgctgc ttctctctgc cttctggag 500

gtgccctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

agagcacccgg cagatccccag tncaaagtct ttgacccttg ctgaatctga 50

gcagcacatt ncaagcaacc ccttgcccttg aaggtggttt ncatcccccc 100

tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250

tatggcaata gnatnnttcg nggnntctat gaccctatga ccccagtcaa 300

tgccaggtac gaatttggtc aggctctttt cactggctgg gctgctgctt 350

ctctctgcct tctgggaggt gccctactttt gctgttccttg tccccgaa 398

<210> 276

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<223> unknown base

<400> 276

agcaatgcccg tgcccccagt ggaggattaa ttccttatgnt ggggacaaca 50

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cagagcacccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcacatttcc 200

tgggagtgat agcaatctttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttggaaac acgatgagg gcagaagatg aggatggctg tcattgggg 300

cgcgatattttt ctntttgcag gtctggctat ttttagttgcc acagcatgg 350

atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttggtaa ggctttnttc actggctggg ctgctgctn 450  
tttctgcctt ntgggaggta ccctantttg ctgttcctgc gaacc 495

<210> 277  
<211> 200  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 34, 87, 138, 147, 163, 165-166, 172  
<223> unknown base

<400> 277  
tcataggggg ggcgcatatt ttttcttgc ggtntggta tttagttgc 50  
cacagcatgg tatggcaata gaatcggtca agaattntat gaccctatga 100  
ccccagtcaa tgccaggtac gaatttggtc aggctctttt cactggntgg 150  
gctgctgctt ctntnngcct tntgggaggt gccctactttt gctgttcctg 200

<210> 278  
<211> 542  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396  
<223> unknown base

<400> 278  
ttcctggat ggatccgccc ccatcntcac atgccttgcc ccntggagat 50  
ttacncctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100  
gggctgtgga atgtcctgcg tgtcccagag cacccggcag atccagtgc 150  
aagtcttga ctccttgctg aatctgagca gcacattgca agcaaccntg 200  
ccttgcgtggat ggttggcatc ctcctggagat tgatagcaat ctttgtggcc 250  
accgttggca tgaaagtgtt tgaagtgcattt ggaagacgat gaggtgcaga 300  
agatgaggat ggctgtcatt gggggcgcga tatttcttct tgcaggtctg 350  
gctatttttag nngccacagc atggtatgca aatcagaccc nntcanaaac 400  
tctatgaccc tatgacccca gtcaatgcca ggtacgaattt tggtcaggct 450  
ctcttcactg gctgggctgc tgcttcttc tgccttctgg gaggtgcct 500  
actttgctgt tcctgtcccc gaaaaacaac ctcttaccca cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
cggggctgca gctgttggc ttcatctcg ttcctggat ggaatcggcg 50  
ccatcgtag cactgccctg ccccatggag gatttactcn tatgctggcg 100  
acaacatcgat gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcagag caccggcag atccagtgc aagtcttga ctcccttgctg 200  
aatctgagca gcacattgc acaaccntg ctttgatggt gttggcattc 250  
ctcctggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgcattt gaagacgatg aggtgcagaa gatgaggatg gctgtcattt 350  
ggggcgcgat atttcttctt gcaggtctgg ctattntag ttgccacagc 400  
atggtatggc aatagaatcg ttcaagaattt ctatgaccct atgaccggcag 450  
tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500  
gcttctctct gccttctggg aggtgcccta ctggctgtt cctgcgaa 548

<210> 280  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 280  
cgagcgagtc atggccaacg c 21

<210> 281  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 281  
gtgtcacacag tagtcttcc cgctgg 26

<210> 282  
<211> 43

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 282  
ctgcagctgt tgggcttcat tctcgcccttc ctggatgga tcg 43

<210> 283  
<211> 2285  
<212> DNA  
<213> Homo sapiens

<400> 283  
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ctgcgcctgc accgcgtaga ccgacccccc cctccagcgc gcccacccgg 100  
tagaggaccc ccgcccggtc cccgaccggt cccgccttt ttgtaaaact 150  
taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200  
ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250  
ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300  
ccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350  
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400  
caacagcgga atcatcgatg caggggcctc aattaatgta tctgtatgt 450  
tacagcctt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
gttcagtcta tgttgctcc aactgacact tcagatatgg aagcagtatg 550  
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgt 600  
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650  
attatatcca caactgcac 700  
tctgagttct tctttggatg acaccgaagt taagaaggaaat 750  
gtaagaggct gcaagggtgaa gttcagaggc tacgggagga gaacaagcag 800  
ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
ccccatttca gcattagccc caactggaa ggaagaaggc cttagcaccc 900  
ggctcttggc tctgggggtt ttgttcttta tcgttggtgt aattattggg 950  
aagattgcct tgttagaggta gcatgcacag gatgttaat tggattggtg 1000  
gatccaccat atcatggat ttaaatttat cataaccatg tgaaaaaga 1050

aattaatgta tgatgacatc tcacaggctc tgcctttaaa ttaccctcc 1100  
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150  
ttagaaagtt aaaaatgtat agtaactgat tgaggggaa aaagaatgat 1200  
ctttattaaat gacaaggaa accatgagta atgccacaat ggcatttgt 1250  
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300  
tctcttaaaa tgacaccctt cctcgctgt tggtgctggc ccttgggag 1350  
ctggagccc gcatgctggg gagtgcggtc agctccacac agtagtcccc 1400  
acgtggccca ctcccgcccc aggctgctt ccgtgtcttc agttctgtcc 1450  
aagccatcag ctccctggga ctgatgaaca gagtcagaag cccaaaggaa 1500  
ttgcactgtg gcagcatcag acgtactcgt cataagttag aggcgtgtgt 1550  
tgactgattt acccagcgct ttggaaataa atggcagtgc tttgttact 1600  
taaaggacc aagctaaatt tgtattgggt catgtatg agtcaaactg 1650  
ttattcagag atgttaatg cataattaaac ttatttaatg tatttcatct 1700  
catgtttct tattgtcaca agagtagt taatgctgctg tgctgctgaa 1750  
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ctctggagag tctggtcatg tggaggtggg gtttattggg atgctggaga 1850  
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tgaagagtag tcagtcttct agattgttct tataaccacct ctcaaccatt 2000  
actcacactt ccagcgcccc ggtccaagtc tgagcctgac ctcccttgg 2050  
ggacctagcc tggagtcagg acaaattggat cgggctgcag agggtagaa 2100  
gcgagggcac cagcagttgt gggggggag caagggaga gagaaactct 2150  
tcagcgaatc cttcttagtac tagttgagag tttgactgtg aattaatttt 2200  
atgccataaa agaccaaccc agttctgttt gactatgtag catctgaaa 2250  
agaaaaattta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

1	5	10	15
Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu			
	20	25	30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys			
	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile			
	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro			
	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val			
	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val			
	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg			
	110	115	120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val			
	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr			
	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu			
	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val			
	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly			
	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala			
	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu			
	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys			
	230	235	240
Ile Ala Leu			

<210> 285  
<211> 418  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255  
<223> unknown base

<400> 285  
gtcagtcttc tagattgtcc ttatcccacc tttcaaccan tactcacatt 50  
  
tcnagcgccc aggtccangt ctgagcctga cttcccttg gggacctagc 100  
ctggagtcag gacaatggnt cgggctgcag aggnttagaa gcgagggcac 150  
cagcagttt gggggggag caagggnnga gagaaactct tcagcgaatc 200  
cttctagtagc tagttgagag tttgactgtg aattaatttt atgccataaa 250  
agacnaaccc agttctgttt gactatgtag catctgaaa agaaaaattta 300  
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgc 350  
ctatgggggg aattattatt ttatcatttt tattatttg ccattggaag 400  
gttaacttta aaatgagc 418

<210> 286  
<211> 543  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 73, 97  
<223> unknown base

<400> 286  
tattgtaaag gccattttaa accattggta ggccttggta catgatgctg 50  
  
gattacctcc ttAAATgaca ccNTTcCTcg CCTGTTGGTg CTGGCCNTG 100  
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggcccactcc cggcccaggc tgcttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgcttg gaaataaatg gcagtgcTTT 350  
gttcaactaa agggaccaag ctaaattgta ttggTTcatg tagtgaagt 400  
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450  
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
gctgaactct gttgggtgaa ctggattgc tgctggaggg ctg 543

<210> 287  
<211> 270

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242  
<223> unknown base

<400> 287  
ccctgggtt tttgttcttt aattcggtgg tgtaattttt gggaaaggattg 50  
ctttagagg tagnatgcac cnggctggta aattggattt gtggatccac 100  
catatccatg ggatataat ttatcataac catgtgtaaa aagaaattaa 150  
tgtatgtga catntcacag gtattgcctt taaattaccc atccctgnan 200  
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
agttaaaaat gtatagtaac 270

<210> 288  
<211> 428  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351  
<223> unknown base

<400> 288  
ggtggcccat tccccggccca ggctgctttc cggtnttcag ttctgtccaa 50  
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgtt 150  
actgattgac ccagcgcttt gcaaataaat ggcagtgcctt tgttcantta 200  
aagggaccaa gctaaatttg tattggttca tgttagtgaag tcaaactgtt 250  
attcagagat gttaatgca tatttaantt atttaatgtt tttnatntca 300  
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
ntgttgggtt aactggattt gctgctggag ggctgtgggc tcctctgtct 400  
ttggagagtc tggtcatgtg gaggtggg 428

<210> 289  
<211> 320  
<212> DNA  
<213> Homo sapiens

<400> 289  
tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattt cactgtggca gcatcagacg 100  
tactcgcat aagttagagg cgtgtttttt ctgatttacc cagcgctttt 150  
gaaataaatg gcagtgcctt gtttacttaa agggaccaag ctaaatttgt 200  
attggttcat gtagtgaagt caaactgtta ttcagagatg ttatgcatt 250  
atttaactta ttatgttat ttcatctcat gttttttttt tgtcacaaga 300  
gtacagttaa tgctgcgtgc 320  
  
<210> 290  
<211> 609  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> unsure  
<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
447, 481, 513, 532, 584, 598  
<223> unknown base  
  
<400> 290  
aaaccttaa aagtttaggg gaaaagaatg atcctttatt aatgacaagg 50  
gaaaccntgn gtaatgccac aatggcatat tgtaaatgtc attttaaaca 100  
ttggtaggcc ttggtacatg atgctggatt acctcttta aatgacacc 150  
cttcctcgcc tgggttgct ggcccttggg gagctngagc ccagcatgct 200  
ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantccgg 250  
cccaggctgc ttccgtgtc ttcaagttctg tccaagccat cagctccttg 300  
ggantgatga acagagtcag aagccaaag gaattgcant gtggcagcat 350  
cagangtant ngtcataagt gagaggcgtg tggtgantga ttgacccagc 400  
gctttggaaa taaatggcaq tgctttgttc anttaaaggg nccaagntaa 450  
atttgtattt gttcatgttag tgaagtcaaa ntgttattca gagatgtttt 500  
atgcataattt aanttattta atgtatttca tntcatgttt tcttattgtc 550  
acaagggtac agttaatgtc gcgtgcgtc gaantctgtt gggtgaantg 600  
gtattgctg 609  
  
<210> 291  
<211> 493  
<212> DNA  
<213> Homo sapiens  
  
<400> 291

gccccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50  
cacagtagtc cccacgtggc ccactcccg cccaggctgc tttccgtgtc 100  
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
aagccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200  
gagaggcgtg tggtgactga ttgacccagc gctttggaaa taaatggcag 250  
tgcttggttc acttaaaggg accaagctaa atttgttattg gttcatgttag 300  
tgaagtcaaa ctgttattca gagatgtta atgcatattt aacttattta 350  
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400  
gcgtgctgct gaactctgtt gggtgaactg gtattgctgc tggagggctg 450  
tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaaatc atcgatgcag gggcctcaat taatgttatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295  
gcgagctccg ggtgctgtgg cccggccttg gcggggcgcc ctccggctca 50  
ggctggctga gaggctccca gctgcagcgt ccccgccccgc ctccctcgaaa 100  
gctctgatct cagctgacag tgccctcgaa gaccaaacaacaa gcctggcagg 150  
gtctcacttt gttgcccagg ctggagttca gtgccatgtat catggtttac 200  
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctggact 250  
acaggacaaa attagaagat caaaaatggaa aatatgctgc tttgggttat 300  
attttcacc cctgggtgga ccctcatttgaa tggatctgaa atggaaatggg 350  
attttatgtg gcacttgaga aaggtacccc ggattgtcag taaaaggact 400  
ttccatctca ccagccccgc atttggca gatgctaaga tgatggtaaa 450  
tacagtgtgt ggcattcgaaat gccagaaaaga actccaaact cccagcctt 500  
ctgaatttggaa ggattatctt tcctatgaga ctgtcttga gaatggcacc 550  
cgaaccttaa ccagggtgaa agttcaagat ttgggtcttg agccgactca 600  
aaatatcacc acaaagggag tatctgttag gagaaagaga caggtgtatg 650  
gcaccgacag caggttcagc atcttggaca aaaggttctt aaccaatttc 700  
ccttcagca cagctgtgaa gcttccacg ggctgttagtg gcattctcat 750  
ttcccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaagg 800  
actatgtcaa agggagtaaa aagctaagg tagggttggtaa gaagatgagg 850  
aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900  
agcttagtgtt ggtgaccaaaa gagagggtac cagagagcat ctgcaggaga 950  
gagcgaaggg tgggagaaga agaaaaaaat ctggccgggg tcagaggatt 1000  
gccgaaggga ggccttcctt tcagtggacc cgggtcaaga atacccacat 1050  
tccgaagggc tgggcacgag gaggcatggg ggacgctacc ttggactatg 1100  
actatgctct tctggagctg aacgcgtgctc acaaaaagaa atacatggaa 1150  
cttggaatca gcccaacgat caagaaaatg cctggtgaa tgatccactt 1200  
ctcaggattt gataacgata gggctgatca gttggtctat cggttttgc 1250  
gtgtgtccga cgaatccaaat gatctcctt accaatactg cgtatgctgag 1300  
tcgggctcca ccgggttcggg ggtctatctg cgtctgaaag atccagacaa 1350  
aaagaattgg aagcgcaaaa tcattgcggt ctactcaggc caccagtggg 1400

tggatgtcca cggggttcag aaggactaca acgttgctgt tcgcacact 1450  
ccccctaaaat acgcccagat ttgcctctgg attcacggga acgatgccaa 1500  
ttgtgcttac ggctaacaga gacctgaaac agggcggtgt atcatctaaa 1550  
tcacagagaa aaccagctct gcttaccgta gtgagatcac ttcataaggtt 1600  
atgcctggac ttgaactctg tcaatagcat ttcaacattt ttcaaaatca 1650  
ggagattttc gtccatttaa aaaatgtata ggtgcagata ttgaaactag 1700  
gtgggcactt caatgccaag tatatactct tctttacatg gtgatgagtt 1750  
tcattttag aaaaattttg ttgccttctt aaaaatttga cacactttaa 1800  
accttcaaacc aggtattata aataacatgt gactccttaa tggacttatt 1850  
ctcagggtcc tactctaaga agaatctaattt aggtgctgg ttgtgtatta 1900  
aatgtgaaat tgcatagata aaggttagatg gtaaagcaat tagtacaga 1950  
atagagacag aaagttacaa cacagttgtt actactctga gatggatcca 2000  
ttcagctcat gccctcaatg tttatattgt gttatctgtt gggctggga 2050  
cattttagttt agttttttt aagaattaca aatcagaaga aaaagcaagc 2100  
attataaaca aaactaataa ctgtttact gcttaagaa ataacaatta 2150  
caatgtgtat tatttaaaaa tgggagaaat agtttgtct atgaaataaa 2200  
cctagtttag aaatagggaa gctgagacat tttaagatct caagttttta 2250  
tttaactaat actcaaataa tggacttttc atgtatgcat agggaaagaca 2300  
cttcacaaat tatgaatgtt catgtgttga aagccacattt attttatgct 2350  
atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400  
tcttttcaa gaaagagtct ttttctcctt gacaaaatcc agctttgtt 2450  
tgaggactat agggtaattt ctctgattttt taatttttaga tatgtccttt 2500  
cctaaaaatg aataaaatggaaatg aataaatatga 2530

<210> 296  
<211> 413  
<212> PRT  
<213> Homo sapiens

<400> 296  
Met Glu Asn Met Leu Leu Trp Leu Ile Phe Phe Thr Pro Gly Trp  
1 5 10 15

Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

	20	25	30
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu			
35	40	45	
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr			
50	55	60	
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu			
65	70	75	
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn			
80	85	90	
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu			
95	100	105	
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg			
110	115	120	
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp			
125	130	135	
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu			
140	145	150	
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu			
155	160	165	
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly			
170	175	180	
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser			
185	190	195	
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala			
200	205	210	
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu			
215	220	225	
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln			
230	235	240	
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys			
245	250	255	
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp			
260	265	270	
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala			
275	280	285	
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys			
290	295	300	
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp			

	305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu			
320	325		330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser			
335	340		345
Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys			
350	355		360
Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp			
365	370		375
Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg			
380	385		390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly			
395	400		405
Asn Asp Ala Asn Cys Ala Tyr Gly			
410			

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catcggtccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaaggggaggc cttcccttca gtggacccgg gtcaagaata cccac 45

<210> 300

<211> 1869  
<212> DNA  
<213> Homo sapiens

<400> 300  
aatgtgagag gggctgatgg aagctgata g caggactgg agtgttagca 50  
ccagtactgg atgtgacagc aggagagga g cacttagca gcttattcag 100  
tgtccgattc tgattccggc aaggatcaa gcatggaatg ctgccgtcg 150  
gcaactcctg gcacactgct cctcttcgt gcttcctgc tcctgagttc 200  
caggaccgca cgctccgagg aggaccggg cggcctatgg gatgcctggg 250  
gccccatggag tgaatgctca cgcacactgct ggggaggggc ctcctactct 300  
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350  
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400  
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagtttat 450  
gaatggcttc ctgtgtctaa tgaccctgac aaccatgtt cactcaagtg 500  
ccaagccaaa ggaacaaccc tgggtgttga actagcacct aaggtcttag 550  
atggtacgct ttgctataca gaatcttgg atatgtcat cagtggttta 600  
tgccaaattt tgggtgcga tcaccagctg ggaagcaccc tcaaggaaga 650  
taactgtggg gtctgcaacg gagatgggtc cacctgccc gttggccgag 700  
ggcagtataa atcccagctc tccgcaacca aatcgatga tactgtggtt 750  
gcacttccct atgaaatgtt acatattcgc cttgtctaa aaggtcctga 800  
tcacttatac ctggaaacca aaaccctcca gggactaaa ggtgaaaaca 850  
gtctcagctc cacaggaact ttccttgg acaattctag tgtggacttc 900  
cagaaattt cagacaaaga gatactgaga atggctggac cactcacagc 950  
agatttcatt gtcaagattc gtaactcggt ctccgctgac agtacagtcc 1000  
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tttccttgc tggaggaggt tatcagctga catcggttga 1100  
gtgctacgt ctgaggagca accgtgtggt tgctgacca tactgtcact 1150  
attacccaga gaacatcaa cccaaaccc agcttcagga gtgcaacttg 1200  
gatccttgc tggaggaggt tatcagctga catcggttga 1250  
ctaccatccc cttccctcggt gggaggccac cccatggacc gcgtgctcct 1300

cctcgtgtgg gggggcata cagagccggg cagttcctg tgtggaggag 1350  
gacatccagg ggcatgtcac ttcagtggaa gagtgaaat gcatgtacac 1400  
ccctaagatg cccatcgac agccctgcaa cattttgac tgccctaaat 1450  
ggctggcaca ggagtggtct ccgtgcacag tgacatgtgg ccagggcctc 1500  
agataccgtg tggtcctctg catcgaccat cgaggaatgc acacaggagg 1550  
ctgttagccca aaaacaaagc cccacataaa agaggaatgc atcgtaccca 1600  
ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcc 1650  
tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700  
gccctcgtaa gttgtaaaag cacagactgt tctatattt 1750  
gtttaaagaa agcagtgtct cactggtgt agcttcatg gttctgaac 1800  
taagtgtaat catctcacca aagttttt gctctcaa 1850  
ttagttcaa aaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
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Leu	Ala	Phe	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu	
			20				25					30		
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
				35				40				45		
Ser	Arg	Thr	Cys	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys	
				50			55				60			
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
					65			70				75		
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
				80			85				90			
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
				95				100				105		
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
				110				115				120		
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
				125				130				135		

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp  
140 145 150

Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln  
155 160 165

Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly  
170 175 180

Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln  
185 190 195

Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr  
200 205 210

Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu  
215 220 225

Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser  
230 235 240

Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp  
245 250 255

Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro  
260 265 270

Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala  
275 280 285

Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg  
290 295 300

Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly  
305 310 315

Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn  
320 325 330

Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile  
335 340 345

Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro  
350 355 360

Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His  
365 370 375

Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser  
380 385 390

Ser Cys Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu  
395 400 405

Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys  
410 415 420

Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys Asn Ile Phe  
425 430 435

Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys Thr Val  
440 445 450

Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asp  
455 460 465

His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro  
470 475 480

His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro  
485 490 495

Lys Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln  
500 505 510

Ala Gln Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser  
515 520 525

<210> 302  
<211> 1533  
<212> DNA  
<213> Homo sapiens

<400> 302  
cggacgcgtg ggcggcggt gcggaaactcc cgtggagggg ccgggtggcc 50  
ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100  
ctgggcgggg cgctgtggct ggccggccgc cggttcgtgg ggcccagggt 150  
ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaaagactg 200  
tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgcccag 250  
ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300  
cgccgaggag gcggcggtc agctccgcg cgagctccgc caggccgcgg 350  
agtgcggccc agagcctggc gtcagcgggg tggcgagct catagtcgg 400  
gagctggacc tcgcctcgct gcgcctcggt cgccgccttct gccagggaaat 450  
gctccaggaa gagccttaggc tggatgtctt gatcaataac gcagggatct 500  
tccagtgcctt ttacatgaag actgaagatg ggtttgagat gcagttcgga 550  
gtgaaccatc tggggactt tctactcacc aatcttctcc ttggactcct 600  
caaaagttca gctcccgca ggattgtggt agtttcttcc aaactttata 650  
aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700  
aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgtgc 800  
atcctggtat tgtacggaca aatctgggaa ggcacataca cattccactg 850  
tttgtcaaac cactctcaa ttttgtgtca tgggctttt tcaaaaactcc 900  
agtagaaggt gcccagactt ccatttattt ggcctttca cctgaggtag 950  
aaggagtgtc aggaagatac tttgggatt gttaagagga agaactgttgc 1000  
cccaaagcta tggatgaatc tggtcaaga aaactctggg atatcagtga 1050  
agtgatggtt ggctgctaa aataggaaca aggagtaaaa gagctgttta 1100  
taaaaactgca tatcatgttat atctgtgatc aggaatggtg tggattgaga 1150  
acttgttact tgaagaaaaa gaattttgat attgaaatag cctgctaaga 1200  
ggtacatgtg ggtattttgg agttactgaa aaattatttt tggataaga 1250  
gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
aagtacaatg aaaaatacaa ttatattgtaa attataac tggcaagca 1350  
tggatgacat attaatattt gtcagaatata agtgactcaa agtgctatcg 1400  
agaggaaaaa caagtatctt tgagttcat ggccaaagtg ttaacttagtt 1450  
ttactacaat gtttgggttt tgggtggaaa ttatctgcct ggtgtgtc 1500  
cacaagtctt acttggataa aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly  
1 5 10 15

Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln  
20 25 30

Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr  
35 40 45

Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly Arg Ala Thr Ala  
50 55 60

Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met Gly Cys Arg  
65 70 75

Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg Arg Glu  
80 85 90

Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser Gly

95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg		
110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg		
125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr		
140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His		
155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Gly Leu Leu Lys		
170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr		
185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser		
200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile		
215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val		
230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly		
245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu		
260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr		
275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly		
290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala		
305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val		
320	325	330
Met Val Gly Leu Leu Lys		
335		

<210> 304  
<211> 521  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50  
gcaagaaaaat tntggatata cagtgaagt atggtngcc tgctaaaata 100  
ggaacaagga gtaaaagacg tgtttataaa actgcatac agttatatct 150  
gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
tttgatattt gaatagcctg ntaagaggna catgtggta tttggagtt 250  
actgaaaaat tattttggg ataagagaat ttcagcaaag atgtttaaa 300  
tatataatgt aagtataatg aataataagt acaatgaaaa atacaattat 350  
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
gaattaatgt actcaaagtg ctatcgagag gttttcaag tatcttgag 450  
tttcatggcc aaagtgttaa ctagtttac tacaatgtt ggtgttg 500  
tgaaaattat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccagggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcaggg a tcttccagt g cccttacat g aagactgaag atggg 45  
<210> 308  
<211> 1523  
<212> DNA  
<213> Homo sapiens  
  
<400> 308  
gagaggac ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50  
cgagccccag cccttccta acccaacc a acctagccc gtcggccg 100  
ccagcgcctg tccctgtcac ggacccca gttaccatgc atcctgccgt 150  
cttcctatcc ttacccgacc tcagatgctc cttctgctc ctggtaactt 200  
gggttttac tcctgtaaca actgaaataa caagtctgc tacagagaat 250  
atagatgaaa tttaaacaa tgctgatgtt gcttagtaa atttttatgc 300  
tgactggtgt cgtttcagtc agatgttgc tccaattttt gaggaagctt 350  
ccgatgtcat taaggaagaa ttccaaatg aaaatcaagt agtgttgcc 400  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450  
caaataccca accctcaa at tttcgtaa tggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaatg accccattca agaaattcg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaagaa atatcattgg atatttgag caaaaggact 650  
cgacacta tagatttt gaacgagtag cgaatattt gcatgatgac 700  
tgtgccttc tttctgcatt tggatgatg tcaaaaccgg aaagatata 750  
tggcacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800  
tgtacttggg agctatgaca aatttgatg tgacttacaa ttggattcaa 850  
gataaatgtt ttccttgc tggatgatg acatttggaa atggagaggg 900  
attgacagaa gaaggactgc ctttctcat actcttcac atgaaagaag 950  
atacagaaag tttagaaata ttccagaatg aagtagctg gcaattaata 1000  
agtaaaaaag gtacaataaa cttttacat ggcgattgtg acaaatttag 1050  
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag cttaggcat atgtatgtt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaaactgat acagccccag 1250

gagagcaagc ccaagatgt a gcaaggagtc cacctgagag ctccttccag 1300  
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
gctttaaaaa cttgaaaaac agtttgtaag ccttcaaca gcagcatcaa 1400  
cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309

<211> 406

<212> PRT

<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser
1				5				10					15	
Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu
				20				25					30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn
				35				40					45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe
				50				55					60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile
				65				70					75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val
				80				85					90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser
				95				100					105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys
				110				115					120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr
				125				130					135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu
				140				145					150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly
				155				160					165	
Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg
				170				175					180	
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe
				185				190					195	

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile  
200 205 210

Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly  
215 220 225

Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys  
230 235 240

Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu  
245 250 255

Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys  
260 265 270

Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg  
275 280 285

Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp  
290 295 300

Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro  
305 310 315

Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr  
320 325 330

Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys  
335 340 345

Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe  
350 355 360

His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala  
365 370 375

Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu  
380 385 390

Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu  
395 400 405

Leu

<210> 310  
<211> 182  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 36, 48  
<223> unknown base

<400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtnttg ccagagtnga 50  
ttgtgatcg cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgttcgt aatggatga tcatgaagag agaatacagg 150  
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311  
<211> 598  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396  
<223> unknown base

<400> 311  
agaggcctct ctgaaagttg tcccgggtgt tcgcgcngg agcccggtc 50  
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100  
cgagccccag cccttccta acccaaccca acctagccn gtcccagccg 150  
ccagcgccctg tccctgtcnc ggancggcgc gtnaccatgc atcctggcgt 200  
cttcctatcc ttacccgacc tcagatgctc cttctgctc ctggtaactt 250  
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaaacna tgctgatgtg gctttagtca attttatgc 350  
tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangtt 400  
ccgatgtcat taaggaagaa ttccaaatg aaaatcaagt agtggggcc 450  
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 500  
caaataaccca accctcaaat tgttcgtaa tggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 312  
tgagaggcct ctctgaaagt tg 22

<210> 313  
<211> 19  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313  
gtcagcgatc agtcaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314  
ccagaatgaa gtagtcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315  
ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316  
catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317  
ggtgctatacg gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 318  
ctgttatctc gggctatgtc agag 24

<210> 319  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 319  
ctacatataa tggcacatgt cagcc 25

<210> 320  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 320  
cgctttccta tccttacccg acctcagatg ctcccttctg ctcttg 46

<210> 321  
<211> 1333  
<212> DNA  
<213> Homo sapiens

<400> 321  
gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50  
cgctgctgct cactgccgca ctcatcttct tcgcatttg gcacattata 100  
gcatttgatg agctgaagac tgattacaag aatccatag accagtgtaa 150  
taccctgaat ccccttgtac tcccagagta cctcatccac gctttcttct 200  
gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250  
ccccctttgg catatcatat ttggaggat atgagtagac cagtgtatg 300  
tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350  
catattgtca gaaggaagga tggtgcaa at tagctttta tcttctagca 400  
ttttttact acctatatgg catgatctat gtttggta gctcttagaa 450  
caacacacag aagaatttgtt ccagttaagt gcatgcaaaa agccacaaaa 500  
tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550  
tgatcagtta cttaaaaaaaaa tgactcctta ttttttaat gtttccacat 600

tttgcttgt ggaaagactg tttcatatg ttatactcg ataaagattt 650  
taaatggtat tacgtataaa ttaatataaa atgattacct ctgggttgta 700  
caggttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
gcattaatta ctgactgtcc tagtacattg gaagctttg tttataggaa 800  
ctttagggc tcatttttgt ttcattgaaa cagtatctaa ttataaatta 850  
gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900  
tggaaactt catgggttcc ctcatctgatc atgtcgatga ttatatatgg 950  
atacatttac aaaaataaaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
tccctgtata ttgcataat gagagatttc ccataattcc atcagagtaa 1050  
taaatatact tgcttaatt cttaagcata agtaaacatg atataaaaaat 1100  
atatgctgaa ttacttgta agaatgcatt taaagctatt ttaaatgtgt 1150  
ttttatgtt aagacattac ttattaagaa attggttatt atgcttactg 1200  
ttctaattctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250  
tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
gtgcaataca ataaaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu  
1 5 10 15

Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala  
20 25 30

Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys  
35 40 45

Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala  
50 55 60

Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu  
65 70 75

Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met  
80 85 90

Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr  
95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
110 115 120  
  
Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
125 130 135  
  
Gly Met Ile Tyr Val Leu Val Ser Ser  
140

<210> 323  
<211> 477  
<212> DNA  
<213> Homo sapiens

<400> 323  
attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100  
cttctgtgtc atgttcttt gtgcagcaga gtggcttaca ctgggtctca 150  
atatccccct cttggcatat catattgga ggtatatgag tagaccagt 200  
atgagtggcc caggactcta tgaccctaca accatcatga atgcagat 250  
tctagcatat tgtcagaagg aaggatggtg caaatttagct ttttatcttc 300  
tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350  
tagaacaaca cacagaagaa ttggtccagt taagtgcattg caaaaagcca 400  
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
gaatctgatc agttacttta aaaaatg 477

<210> 324  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 324  
tgtaaaaacgca cggccagttt aatagacctg caattattaat tct 43

<210> 325  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 325  
caggaaacagat ctagaccac ctgcacacccat gcaaattttt t 41

<210> 326  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tggtgcaaat tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg gggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggacaaga tggcgccgcgaa agggggagc ctctgggtga 100  
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150  
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200  
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcattgc agagaggtt caggctgttt 300  
tcaatttgtc agtttggaa tgatgaaatt gacttaaatc gaactaaatt 350  
ggaatgtgaa tctgcattgtc cagaagcata ttcccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tcttcctct 500  
aactctggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550  
tcataacctc ttcatggact ttttatcttc aagccgatga cgaaaaata 600  
gttatattcc agtctaagcc agaaatccag tacgcaccac atttggagca 650  
ggagcctaca aattttagag aatcatctct aagcaaaatg tcctatctgc 700  
aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
gatggcttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
aactcttgc tcctcggtgta tggatttgct ttggatttgt tgtgcaactg 850  
ttgctacagc tgtggaggcag tatgttccct ctgagaagct gagtatctat 900  
ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
ttctcttgc gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcattttc 1050  
ttttaaaaga caagtgtaat agacatctaa aattccactc ctcatalogc 1100  
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
caaataaaagt tactcaaatac tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10				15	

Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
							20			25			30	

Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
					35				40				45	

Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
				50				55				60		

Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
					65				70			75		

Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
					80			85				90		

Arg	Thr	*Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
					95				100			105		

Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln  
110 115 120

Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met  
125 130 135

Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe  
140 145 150

Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser  
155 160 165

Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe  
170 175 180

Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu  
185 190 195

Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu  
200 205 210

Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly  
215 220 225

Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp  
230 235 240

Ile Leu Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp  
245 250 255

Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro  
260 265 270

Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu  
275 280 285

Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg  
290 295 300

Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys  
305 310 315

Val Asn Leu Ala His Ser Glu Ile  
320

<210> 331  
<211> 350  
<212> DNA  
<213> Homo sapiens

<400> 331  
ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctacccctt 50  
gcacacctac cctaaggaag aggagttgta cgcatgtcag agaggttgca 100  
ggctgttttc aatttgtcag tttgtggatg atgaaattga cttaaatcga 150

actaaattgg aatgtgaatc tgcatagtaca gaagcatatt cccaatctga 200  
tgagcaatat gcttgcacatc ttggttgcca gaatcagctg ccattcgctg 250  
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
tttcctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350  
<210> 332  
<211> 562  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> unsure  
<222> 47  
<223> unknown base  
  
<400> 332  
cacactggcc ggatctttta gagtccttg accttgacca agggtcngga 50  
aacacgcaac aagctgagct gctgtgacag agggaaacaag atggcggcgc 100  
cgaagggagc ctttgggtga ggacccaact ggggctcccgg ccgctgctgc 150  
tgctgaccat ggccttggcc ggagggttcgg ggaccgcttc ggctgaagca 200  
tttgactcgg tcttgggtga tacggcgctc tgccaccggg cctgtcagtt 250  
gacctacccc ttgcacacacct accctaagga agaggagttg tacgcatgtc 300  
agagaggttg caggctgttt tcaatttgc agtttgtgga tgatggaatt 350  
gacttaaattc gaactaaattt ggaatgtgaa tctgcattgtc cagaagcata 400  
ttcccaatct gatgagcaat atgcttgcga tcttgggtgc cagaatcagc 450  
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500  
atgcacccatc tctttcctct aactctggtg aggtcattct ggagtgacat 550  
gatggactcc gc 562  
  
<210> 333  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 333  
acaagctgag ctgctgtgac ag 22  
  
<210> 334  
<211> 22

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg ccggagggttc ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgagggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cggcccgag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100  
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtgg 150  
gcgacaagct gccggagctg caatggccg cggctggga ttcttgtttg 200  
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
ccccccggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaaccat ttagatgattt aataactaca 350  
ggctttcccc aagactacaa aaacttcttg aaagtgacta cttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttcttggatg acatcagcca 450  
gtgttggaaa agggactgtg ctgtcaaacc atgtcaatct gatgaaggttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600  
tctgagttag gaaacacaga aggctttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgttag atttgcatttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaaga cctttaaatc ctggcggtc tggcaaggg 850  
acaagtgaag agaacacttt ttacagttgg ctagaaggc tctgtgtaga 900  
aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950  
tgcatggag tgcaagatat ctttacaag agacctgggtt agaaaagaaa 1000  
tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
tgaaggagaa ggtccaagaa ggcttaagaa cttgtatccc ctctacttaa 1100  
tagaactaag ggcttatcc aaagtgttac cattttcga ggcggccagat 1150  
tttcaactct ttactggaaa taaaatttag gatgaggaaa acaaaatgtt 1200  
acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250  
agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300  
gactttcgac tgcatggat aaatatttca agaattatgg attgtgttgg 1350  
ttgtttaaa tgtcgctgt gggaaagct tcagacttag ggtttggca 1400  
ctgctctgaa gatcttattt tctgagaaat tgatagcaa tatgccagaa 1450  
agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtattcatt 1500  
attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaaact 1550  
tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
atagcaatga cagtcctaaag ccaaacattt tatataaaatg tgctttgtt 1700  
aaggagaatt atattgtttt aagtaaacac attttaaaa attgtgtttaa 1750  
gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800  
acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1885

<210> 337  
<211> 468  
<212> PRT  
<213> Homo sapiens

<400> 337  
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Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr  
20 25 30

Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp  
35 40 45

Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg  
50 55 60

Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg  
65 70 75

Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp  
80 85 90

Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln  
95 100 105

Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr  
110 115 120

Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu  
125 130 135

Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys  
140 145 150

Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe  
155 160 165

Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp  
170 175 180

Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp  
185 190 195

Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys  
200 205 210

Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln  
215 220 225

Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu  
230 235 240

Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His  
245 250 255

Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu  
260 265 270

Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln  
275 280 285

Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg  
290 295 300

Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu  
305 310 315

Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe  
320 325 330

Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu  
335 340 345

Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu  
350 355 360

Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys  
365 370 375

Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp  
380 385 390

Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr  
395 400 405

Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu  
410 415 420

Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu  
425 430 435

Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile  
440 445 450

Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln  
455 460 465

Asn Ile His

<210> 338

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

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ttaaaagacc tttaaatcct ttggcttctg gtcaaggac aagtgaagag 100

nacactttt acagttggct agaaggtctc tgtgttagaaa aaagagcatt 150

ctacagactt atatctggcc tacatgcaag cattaatgtc catttgagtg 200

caagatatct tttacaagag acctggtagg aaaagaaatg gggcacacaac 250

attacagaat tttaacagcg atttgatgga atttgactg aaggagaagg 300

tccaagaagg cttaagaact tgtatttct ctacttaata gaactaaggg 350

ctttatccaa agtgttacca ttcttngagc gcccagattt tcaactnttt 400  
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttgaaat 450  
acttcatgaa atcaagtcat ttccttgca ttttgatgag aattcatttt 500  
tttgctg 507

<210> 339  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 339  
aagctgccgg agctgcaatg 20

<210> 340  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 340  
ttgcttctta atcctgagcg c 21

<210> 341  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 341  
aaaggaggac ttgcactgc 20

<210> 342  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 342  
agagattcat ccactgctcc aagtgc 26

<210> 343  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 343  
tgtccagaaa caggcacata tcagc 25  
  
<210> 344  
<211> 50  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 344  
agacagcggc acagaggtgc ttctgccagg ttagtggta cttggatgat 50  
  
<210> 345  
<211> 1486  
<212> DNA  
<213> Homo sapiens  
  
<400> 345  
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gatgggaggaa aagtgaaga aaacagaaaa ggagagggac agaggccaga 100  
ggacttctca tactggacag aaaccgatca ggcatttgcac tccccttcgt 150  
cactcacctg ttcttgcccc tgggtttcct gacaggtctc tgctccccct 200  
ttaacctgga tgaacatcac ccacgcctat tcccaggggcc accagaagct 250  
gaatttggat acagtgtctt acaacatgtt ggggtggac agcgatggat 300  
gctggggc gccccctggg atgggccttc aggccaccgg aggggggacg 350  
tttatcgctg ccctgttaggg gggccaca atgcggcatg tgccaagggc 400  
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450  
gcacctgggg atgtctctgt tagagacaga tggtgatggg ggattcatgg 500  
tgagctaagg agagggtggt ggcagtgtct ctgtggatggc ataaaagaaa 550  
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taaaaaaccct agaaagcaa aggttaggtaa tgtcaggag tagtcttcatt 650  
gcctccttca actgggagca tggtctgagg gtgcctccc aagcctggga 700  
gtaactatccccc cccatccc caggcctgtg cccctctctg gtctcgtgt 750  
tgtggcagct ctgtcttcag ttctggata tgtgcccgtg tggatgcttc 800  
atcccagcct caggaaagcc tggcacccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900  
ggccaagcg gtatgatgcc tggcaaaggc cctgcattgc tatcctcatt 950  
gctacctaattgtcttgc aagctccatg tttcctaaca gattcagact 1000  
cctggccagg tgtggtggcc cacacctgta attctagcac ttgggaggc 1050  
caaggtggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100  
catggtaaaa ctccatctct actaaaaaaaaaaaaataca aaaatttagct 1150  
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ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250  
gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300  
aaaataataa taataataat tcagactcct tattcaggagt ccatgatctg 1350  
gcctggcaca gtaactcatg cctgtaatcc caacattttggaggccaac 1400  
gcaggaggat tgcttgaggt ctggagggtt gagaccagcc tggcaacat 1450  
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe	
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Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro	
									20					30	
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val	
									35					45	
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala	
									50					60	
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg	
									65					75	
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His	
									80					90	
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn	
									95					105	
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly	
									110					120	
									115						

Phe Met Val Ser

<210> 347  
<211> 509  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 22  
<223> unknown base

<400> 347  
cacagttccc caccatcaact cntcccattc cttccaactt tatttttagc 50  
ttgccattgg gagggggcag gatgggaggaa aaagtgaaga aaacagaaaa 100  
ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150  
ggcatggaac tccccttcggt cactcacctg ttcttgcccc tggtgttcct 200  
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
tcccaggggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300  
gggggtggac agcgatggat gctggtggc gccccctggg atgggccttc 350  
aggcgaccgg aggggggacg tttatcgctg ccctgttaggg ggggcccaca 400  
atgccccatg tgccaaagggc cacttaggtg actaccaact gggaaattca 450  
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500  
tggtgatgg 509

<210> 348  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 348  
aggcacagag gccagaggac ttc 23

<210> 349  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 349  
caggtgcata ttcacagcag gatg 24

<210> 350  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 350  
ggaaactcccc ttctgtcactc acctgttctt gcccctggtg ttcct 45

<210> 351  
<211> 2056  
<212> DNA  
<213> Homo sapiens

<400> 351  
aaagttacat tttctctgga actctccctag gccactccct gctgatgcaa 50  
catctgggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100  
gcttcctggg ccggctctag aacaatttag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaaatggctgaga tggacagaat 200  
gctttatTTT ggaaagaaac aatgttctag gtcaaactga gtctaccaaa 250  
tgcagacttt cacaatggtt cttagaagaaa tctggacaag tctttcatg 300  
tggTTTTCT acgcattgtat tccatgtttg ctcacagatg aagtggccat 350  
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
tcttgatgtg gagccagtg atcgcgcctg gagaaacagt gtactattct 450  
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atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600  
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700  
acctggttat tgagctggag gacctggggc cccagttga gttccttgt 750  
gcctactgga ggagggagcc tggtgccgag gaacatgtca aaatggtgag 800  
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850  
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ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccctggt 950  
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cactgttcgt ctggaaaatg ggccggctgc tccagtaactc ctgttgcccc 1050  
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aatcagctgc agaaggagg agggtggatgc ctgtgccacg gctgtgatgt 1150  
ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200  
caggtgaagc cgagaacctg gtctgcata catgaaacc atgaggggac 1250  
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gagcctgttg tctacaagtc tagaagcaac catcagaggc agggtggtt 1350  
gtctaacaga acactgactg aggcttaggg gatgtgaccc ctagactggg 1400  
ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcatccctt 1450  
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tacacccagc acttgcaagg ctagaggaa actggtgaca ctctacagtc 1600  
tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650  
gatcaaggac tctacacact gggtggttg gagagccac tttccagaa 1700  
taatccttga gagaaaagga atcatggag caatgggtt gagttcactt 1750  
caagcccaat gccgggtcag agggaaatgg cttagcgagc tctacagtag 1800  
gtgacctgga ggaagggtcac agccacactg aaaatggat gtgcataaac 1850  
acggaggatc catgaactac tgtaaatgt tgacagtgtg tgcacactgc 1900  
agacagcagg tgaaatgtat gtgtcaatg cgacgagaat gcagaagtca 1950  
gtaacatgtg catgtttgtt gtgctcctt tttctgttgg taaagtacag 2000  
aattcagcaa ataaaaaggg ccaccctggc caaaagcggt aaaaaaaaaa 2050  
aaaaaaaa 2056

<210> 352  
<211> 311  
<212> PRT  
<213> Homo sapiens

<400> 352  
Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu  
1 5 10 15  
Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
20 25 30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
35 40 45

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro  
50 55 60

Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu  
65 70 75

Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser  
80 85 90

Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala  
95 100 105

Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln  
110 115 120

Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser  
125 130 135

Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe  
140 145 150

His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe  
155 160 165

Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val  
170 175 180

Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met  
185 190 195

Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys  
200 205 210

Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu  
215 220 225

Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
230 235 240

Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp  
245 250 255

Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val  
260 265 270

Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile  
275 280 285

Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met  
290 295 300

Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser  
305 310

<210> 353  
<211> 864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 654, 711, 748, 827  
<223> unknown base

<400> 353  
tcctgctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50  
cctttctagc ttcctggccg gctctagaac aattcaggct tcgctgcgac 100  
tagacctca gtcacata tgcattctga agaaagatgg ctgagatgac 150  
agaatgcttt atttggaaa gaaacaatgt tctaggtcaa actgagtcta 200  
ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250  
tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
gccattctgc ctgccccctca gaacctctct gtactctcaa ccaacatgaa 350  
gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450  
tggatccccca gcagctggtg ctcactcact gaaggccctg agtgtgatgt 500  
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550  
cattgggctc acagacctca gcctggagca tcctgaagca tcccttaat 600  
agaaaactcaa ccatcctac ccgacctggg atggagatca ccaaagatgg 650  
cttncacctg gttattgagc tggaggacct gggggcccaag tttgagttcc 700  
tttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800  
tgacccacat actcaaatatg gacgaantgc tattgtccac ctgtttgagt 850  
ggcgctgggt tgat 864

<210> 354  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 354  
aggcttcgct gcgactagac ctc 23

<210> 355  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 355  
ccaggtcggg taaggatggt tgag 24

<210> 356  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 356  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357  
<211> 1670  
<212> DNA  
<213> Homo sapiens

<400> 357  
cccacgcgtc cgccccacgcg tccgaggac aagagagaag agagactgaa 50  
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100  
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
agaggcagga gctggaaagg agagaggag gaggaggagg agatgcggga 200  
tggagacctg gagtttaggtg gcttggaga gcttaatgaa aagagaacgg 250  
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300  
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350  
ggaaaagagc agagggaaaga ggaaagacac agagagacgg gagagagaag 400  
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450  
ggaaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500  
ggacagggtc ccagaaggag gggacagagg agctgagaga gggggcagg 550  
gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600  
cgtctgagcg cccctcgagc gctggtaactc tgggctgcac tggggcagc 650  
agctcacatc ggaccagcac ctgaccccgaa ggactgggtgg agctacaagg 700

ataatctcca gggaaacttc gtgccaggc ctccttctg gggcctgg 750  
aatgcagcgt ggagtctgtg tgctgtggg aagcggcaga gccccgtg 800  
tgtggagctg aagagggttc tttatgaccc ct当地tgc当地 ccattaaggc 850  
tcagcactgg aggagagaag ctccgggaa ccttgc当地 aaccggccga 900  
catgtctc当地 tc当地gc当地tgc accccc当地tgc当地 gtggtaatg tgtctggagg 950  
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ctcgac当地gg agccggctcg gaacatcaga tcaaccacca gggcttctc 1050  
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cgctgc当地tcc cgccggccca atggc当地tggc cattctc当地g ct当地ttgtca 1150  
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accatc当地ctc gcatctc当地ta caagaatgt gc当地tacttcc ttcaaggac 1250  
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

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Trp	Ala	Ala	Leu	Gly	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp	
					20				25					30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
					35				40					45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
					50				55					60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu  
65 70 75

Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser  
80 85 90

Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg  
95 100 105

His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser  
110 115 120

Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu  
125 130 135

Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn  
140 145 150

His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln  
155 160 165

Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly  
170 175 180

Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn  
185 190 195

Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile  
200 205 210

Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu  
215 220 225

Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser  
230 235 240

Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile  
245 250 255

Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg  
260 265 270

Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser  
275 280 285

Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg  
290 295 300

Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro  
305 310 315

Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg  
320 325

<210> 359

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 359  
tctgctgagg tgcagtcat tcac 24

<210> 360  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 360  
gaggctctgg aagatctgag atgg 24

<210> 361  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 361  
gcctctttgt caacgttgcc agtacacctta acccattcct cagtcgcctc 50

<210> 362  
<211> 3038  
<212> DNA  
<213> Homo sapiens

<400> 362  
ggcgccctggt tctgcgcgta ctggctgtac ggagcaggag caagaggctg 50  
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gcagctactg ctcagaaacg ctggggcgcc caccctggca gactaacgaa 150  
gcagctccct tcccacccca actgcagggtc taattttgga cgctttgcct 200  
gccatttctt ccaggtttag ggagccgcag aggccggaggc tcgcgtattc 250  
ctgcagtcag cacccacgtc gccccggac gctcggtgct caggcccttc 300  
gcgagcgggg ctctccgtct gcgggtccctt gtgaaggctc tgggcggctg 350  
cagaggccgg ccgtccgggtt tggctcacct ctcccaggaa acttcacact 400  
ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctgggaa 450  
atcctgaggt cattcattat gaagtgtacc gcgcggaggt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550  
atgccactt attggagaaa cttttggaaa aatacatgga tgaggatgg 600  
gagtggtgga tagccaaaca acgaggaaa agggccatca cagacaatga 650  
catgcagagt attttggacc ttcataataa attacgaagt caggtgtatc 700  
caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750  
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tcagacaggt attatcccc tcgagaAGAG gaaACAAATG aaATAGAAACG 1250  
acagcagtca caagtccatg acacCCATGT ccggacaAGA tcagatgata 1300  
gtAGCAGAAA tgaAGTCATA AGCGCACAGC AAATGTCCC AATTGTTCT 1350  
tgtGAAGTAA gattaAGAGA tcAGTGCAA GGAACAACCT GCAATAGGTa 1400  
cgaatgtcct gctggctgtt tggatAGTAa agctAAAGTT attggcAGTG 1450  
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ataatAGACA atgatGGTGG ctgggtAGAT atcactAGAC aAGGAAGAAA 1550  
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atgGAATCTT CTCAGAAAGT ttacAGAAATC ctccAGGAGG aaAGGcATTc 1950

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atTTTTTTC tgctggtgga ttacatatt aaatTTTTC tgctggtgga 3000  
taaacattaa aattaatcat gtttcaaaaa aaaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20					25				30	

Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu  
35 40 45

Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn  
50 55 60

Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln  
65 70 75

Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val  
. 80 85 90

Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp  
95 100 105

Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu  
110 115 120

Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln  
125 130 135

Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His  
140 145 150

Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys  
155 160 165

Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly  
170 175 180

Cys Ala Ile Asn Leu Cys His Asn Met Asn Ile Trp Gly Gln Ile  
185 190 195

Trp Pro Lys Ala Val Tyr Leu Val Cys Asn Tyr Ser Pro Lys Gly  
200 205 210

Asn Trp Trp Gly His Ala Pro Tyr Lys His Gly Arg Pro Cys Ser  
215 220 225

Ala Cys Pro Pro Ser Phe Gly Gly Cys Arg Glu Asn Leu Cys  
230 235 240

Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr Pro Pro Arg Glu Glu Glu  
245 250 255

Thr Asn Glu Ile Glu Arg Gln Gln Ser Gln Val His Asp Thr His  
260 265 270

Val Arg Thr Arg Ser Asp Asp Ser Ser Arg Asn Glu Val Ile Ser  
275 280 285

Ala Gln Gln Met Ser Gln Ile Val Ser Cys Glu Val Arg Leu Arg  
290 295 300

Asp Gln Cys Lys Gly Thr Thr Cys Asn Arg Tyr Glu Cys Pro Ala  
305 310 315

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr  
320 325 330

Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile  
335 340 345

Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg  
350 355 360

Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile  
365 370 375

Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr  
380 385 390

Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro  
395 400 405

Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg  
410 415 420

Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr  
425 430 435

Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His  
440 445 450

Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro  
455 460 465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile  
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg  
485 490 495

Val Phe Ala Val Val  
500

<210> 364  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 364  
ggacagaatt tgggagcaca ctgg 24

<210> 365  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtcctcg 20

<210> 366  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 366  
agcacagatt ttctctacag ccccc 25

<210> 367  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
aaccactcca gcatgtactg ctgc 24

<210> 368  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 368  
ccattcagggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369  
<211> 1685  
<212> DNA  
<213> Homo sapiens

<400> 369  
gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctggcat 50  
ccaccgacgg cgcagccga gccagcagag ccggaaggcg cgccccggc 100  
agagaaaagcc gagcagagct gggtggcgta tccggccgc cgctccgacg 150  
ggccagcgcc ctccccatgt ccctgctccc acgcccgcgc cctccggta 200  
gcatgaggct cctggcgcc gcgctgctcc tgctgctgct ggcgctgtac 250  
accgcgcgtg tggacgggtc caaatgcaag tgctccggaa agggacccaa 300  
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtacccgc 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggta 400  
cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450  
catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500  
agggtgaaaa acctcagaag ggaaaactcc aaaccagttt ggagacttgt 550  
gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600  
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cagtgttgc ccattcctag cttggaaagc ttccgcttag aggtcctggc 950  
gcctcggcac agctgccacg ggctctccctg ggcttatggc cggtcacagc 1000  
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agatcctgtg atggcgagac aaatgatcct taaagaaggt gtggggtctt 1200  
tcccaacctg aggatttctg aaaggttcac aggttcaata ttatgtctt 1250  
cagaagcatg tgaggttccc aacactgtca gcaaaaacct taggagaaaa 1300  
cttaaaaata tatgaataca tgcgcaatac acagctacag acacacattc 1350  
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aaccattagc attgcatgca gtttcataat tctttctaag atggaaagta 1650  
ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370  
<211> 111  
<212> PRT

<213> Homo sapiens

<400> 370

Met Ser Leu Leu Pro Arg Arg Ala Pro Pro Val Ser Met Arg Leu  
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Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala  
20 25 30

Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys  
35 40 45

Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr  
50 55 60

Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val  
65 70 75

Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln  
80 85 90

Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys  
95 100 105

Arg Arg Val Tyr Glu Glu  
110

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 374  
<211> 3113  
<212> DNA  
<213> Homo sapiens

<400> 374  
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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150  
caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200  
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cggtttcagc ccccagaacc cccgtcctcc tggactggca tccgaaatac 300  
tactcagtt gctgctgtgt gcccccagca cctggatgag agatccttac 350  
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gtaatgaccg tggtaagac gaagatattc atgatcagaa cagtaagaag 550  
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<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn	
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Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala	
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Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro	
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Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val	
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Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu	
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Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val	
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Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro	
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Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr	
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Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser  
155 160 165

Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu  
170 175 180

Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly  
185 190 195

Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly  
200 205 210

Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu  
215 220 225

Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly  
230 235 240

Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly  
245 250 255

Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser  
260 265 270

Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu  
275 280 285

Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile  
290 295 300

Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met  
305 310 315

Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln  
320 325 330

Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile  
335 340 345

Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln  
350 355 360

Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly  
365 370 375

Glu Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly  
380 385 390

Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp  
395 400 405

Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr  
410 415 420

Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu  
425 430 435

Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp  
440 445 450

Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser  
455 460 465

Pro Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met  
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Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr  
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Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys  
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Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr  
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Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val  
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Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu  
545 550 555

Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu  
560 565 570

His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr  
575 580 585

Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu  
590 595 600

Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Lys Val Pro Pro  
605 610 615

Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala  
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Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn  
635 640 645

Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp  
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Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu  
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Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile  
680 685 690

Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His  
695 700 705

Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp  
710 715 720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys  
725 730 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp  
740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg  
755 760 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr  
770 775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe  
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His Ser Thr Thr Arg Val  
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<212> PRT  
<213> Homo sapiens

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35 40 45

Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro  
50 55 60

Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met  
65 70 75

Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp  
80 85 90

Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe  
95 100 105

Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln  
110 115 120

Gly Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr  
125 130 135

Lys Asp Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys  
140 145 150

Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu  
155 160 165

Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn  
170 175 180

Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly Arg Pro Thr  
185 190 195

Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His Tyr Asp  
200 205 210

Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile Met  
215 220 225

Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val  
230 235 240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser  
245 250 255

Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys  
260 265 270

Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu  
275 280 285

His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro  
290 295 300

Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe  
305 310 315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val  
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<211> 480  
<212> PRT  
<213> Homo sapiens

<400> 385

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Leu Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile  
20 25 30

Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys  
35 40 45

Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro  
50 55 60

Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu  
65 70 75

Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser  
80 85 90

Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val  
95 ? 100 105

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala  
110 115 120

Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His  
125 130 135

Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser  
140 145 150

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu  
155 160 165

Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu  
170 175 180

Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp  
185 190 195

Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr  
200 205 210

Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe  
215 220 225

Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe  
230 235 240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu  
245 250 255

Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln  
260 265 270

Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro  
275 280 285

Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys  
290 295 300

His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys  
305 310 315

Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu  
320 325 330

Asp Glu Arg Glu Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser  
335 340 345

Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met  
350 355 360

Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr  
365 370 375

Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly  
380 385 390

Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe  
395 400 405

Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg  
410 415 420

Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys  
425 430 435

Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu  
440 445 450

Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly  
455 460 465

Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe  
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<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386  
ccaaggcagct tagagctcca gacc 24

<210> 387  
<211> 25  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 387  
ttcccttatgc tctgtattgg catgg 25

<210> 388  
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<212> DNA  
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<223> Synthetic oligonucleotide probe

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<210> 389  
<211> 3313  
<212> DNA  
<213> Homo sapiens

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aaactctatc tca 3313

<210> 390  
<211> 916  
<212> PRT  
<213> Homo sapiens

<400> 390

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20 25 30

Ile Arg Tyr Ser Val Pro Glu Glu Leu Glu Lys Gly Ser Arg Val  
35 40 45

Gly Asp Ile Ser Arg Asp Leu Gly Leu Glu Pro Arg Glu Leu Ala  
50 55 60

Glu Arg Gly Val Arg Ile Ile Pro Arg Gly Arg Thr Gln Leu Phe  
65 70 75

Ala Leu Asn Pro Arg Ser Gly Ser Leu Val Thr Ala Gly Arg Ile  
80 85 90

Asp Arg Glu Glu Leu Cys Met Gly Ala Ile Lys Cys Gln Leu Asn  
95 100 105

Leu Asp Ile Leu Met Glu Asp Lys Val Lys Ile Tyr Gly Val Glu  
110 115 120

Val Glu Val Arg Asp Ile Asn Asp Asn Ala Pro Tyr Phe Arg Glu  
125 130 135

Ser Glu Leu Glu Ile Lys Ile Ser Glu Asn Ala Ala Thr Glu Met  
140 145 150

Arg Phe Pro Leu Pro His Ala Trp Asp Pro Asp Ile Gly Lys Asn  
155 160 165

Ser Leu Gln Ser Tyr Glu Leu Ser Pro Asn Thr His Phe Ser Leu  
170 175 180

Ile Val Gln Asn Gly Ala Asp Gly Ser Lys Tyr Pro Glu Leu Val  
185 190 195

Leu Lys Arg Ala Leu Asp Arg Glu Glu Lys Ala Ala His His Leu  
200 205 210

Val Leu Thr Ala Ser Asp Gly Gly Asp Pro Val Arg Thr Gly Thr  
215 220 225

Ala Arg Ile Arg Val Met Val Leu Asp Ala Asn Asp Asn Ala Pro  
230 235 240

Ala Phe Ala Gln Pro Glu Tyr Arg Ala Ser Val Pro Glu Asn Leu  
245 250 255

Ala Leu Gly Thr Gln Leu Leu Val Val Asn Ala Thr Asp Pro Asp  
260 265 270

Glu Gly Val Asn Ala Glu Val Arg Tyr Ser Phe Arg Tyr Val Asp  
275 280 285

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr  
290 295 300

Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr  
305 310 315

Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg  
320 325 330

Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro  
335 340 345

Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser  
350 355 360

Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp  
365 370 375

Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu  
380 385 390

Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val  
395 400 405

Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile  
410 415 420

Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu  
425 430 435

Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro  
440 445 450

Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn  
455 460 465

Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp  
470 475 480

Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr  
485 490 495

Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp  
500 505 510

Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe  
515 520 525

Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro  
530 535 540

Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln  
545 550 555

Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp  
560 565 570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly  
575 580 585

Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln  
590 595 600

Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly  
605 610 615

Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg  
620 625 630

Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala  
635 640 645

Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu  
650 655 660

Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu  
665 670 675

Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr  
680 685 690

Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu  
695 700 705

Ala Phe Val Ile Leu Leu Ala Leu Arg Leu Arg Arg Trp His  
710 715 720

Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala  
725 730 735

Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu  
740 745 750

Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys  
755 760 765

Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val  
770 775 780

Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly  
785 790 795

Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser  
800 805 810

Leu Tyr Gln Ile Phe Phe Leu Phe Phe Asn Cys Ser Val Ser  
815 820 825

Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln  
830 835 840

Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn  
845 850 855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr  
860 865 870  
  
Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu  
875 880 885  
  
Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp  
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<210> 391  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 391  
tccgtctctg tgaaccggccc cac 23

<210> 392  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 392  
ctcgggcgca ttgtcgttct ggtc 24

<210> 393  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 393  
ccgactgtga aagagaacgc cccagatcca cttttcccc 40

<210> 394  
<211> 999  
<212> DNA  
<213> Homo sapiens

<400> 394  
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cttggaaagacc tcaccatggg acgccccca cctcgtgcgg ccaagacgtg 200  
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<210> 395  
<211> 260  
<212> PRT  
<213> *Homo sapiens*

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Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro
   35          40          45

Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly
   50          55          60

Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys
   65          70          75

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Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn  
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Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro  
95 100 105

His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp  
110 115 120

Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys  
125 130 135

Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln  
140 145 150

Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu  
155 160 165

Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro  
170 175 180

Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly  
185 190 195

Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly  
200 205 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile  
215 220 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly  
230 235 240

Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile  
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Ile Gly Ser Lys Gly  
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<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 396

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<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaataacct gtggttcagt ccatccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gacgacgtgg aataaagagc tctttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT  
<213> Homo sapiens

<400> 400

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					20				25						30
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
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Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
					50				55						60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
					65				70						75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
					80				85						90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
					95				100						105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
					110				115						120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
					125				130						135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
					140				145						150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
					155				160						165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	
					170				175						180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
					185				190						195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
					200				205						210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
					215				220						225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
					230				235						240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
					245				250						255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
					260				265						270

Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val  
275 280 285

Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg  
290 295 300

Leu Ala Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro  
305 310 315

Tyr His Pro Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu  
320 325 330

Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser  
335 340 345

Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys  
350 355 360

Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly  
365 370 375

Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser  
380 385 390

Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu Pro  
395 400 405

Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser  
410 415 420

Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly  
425 430 435

Ser Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu  
440 445 450

Pro Ser Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val  
455 460 465

Leu Trp Thr Val Leu Gly Pro Cys  
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<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggctgccct gcagttacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402  
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<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

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agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200  
caaaggcaag tccttttc ctttctcctt ttggccttat ctctggcggg 250  
cgccgcggaa cctagaagct attctgttgtt ggaggaaact gagggcagct 300  
ccttgcac caatttagca aaggacctgg gtctggagca gagggaaattc 350  
tccaggcggg gggtaggt tgttccaga gggacaaac tacatttgc 400  
gctcaatcag gagaccgcgg atttgttgtt aaatgagaaa ttggaccgtg 450  
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ctagagagtc cttcgagtt tttcaagct gagctgcaag taatagacat 550  
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tcaaggacaa tggcgagcct ccgcgcgtcgg ccacccgcac gctgcacgtg 2150  
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attttgtggc atttccatgc caatgtttat ttcccccaat ttgtgttat 2650  
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tgaaaaaag tgaacattta cctttattcc tggttctt 2738

<210> 405

<211> 798

<212> PRT

<213> Homo sapiens

<400> 405

Met	Glu	Ala	Ser	Gly	Lys	Leu	Ile	Cys	Arg	Gln	Arg	Gln	Val	Leu	
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Phe	Ser	Phe	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu		
			20					25						30	
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe	
					35				40					45	
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe	
				50					55					60	
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His	
				65					70					75	
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys	
				80					85					90	
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu	
				95					100					105	
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala	
				110					115					120	
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu	
				125					130					135	
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly	
				140					145					150	

Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln  
155 160 165

Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg  
170 175 180

Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu  
185 190 195

Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg  
200 205 210

Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly  
215 220 225

Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala  
230 235 240

Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp  
245 250 255

Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val  
260 265 270

Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala  
275 280 285

Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly  
290 295 300

Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser  
305 310 315

Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly  
320 325 330

Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala  
335 340 345

Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn  
350 355 360

Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp  
365 370 375

Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu  
380 385 390

Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr  
395 400 405

Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr  
410 415 420

Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu  
425 430 435

Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala  
440 445 450

Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser  
455 460 465

Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser  
470 475 480

Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp  
485 490 495

Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn  
500 505 510

Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln  
515 520 525

Gly Phe Gln Phe Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala  
530 535 540

Leu Ser Ser Glu Ala Leu Val Arg Val Val Val Leu Asp Ala Asn  
545 550 555

Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala  
560 565 570

Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu  
575 580 585

Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala  
590 595 600

Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe  
605 610 615

Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu  
620 625 630

Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys  
635 640 645

Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val  
650 655 660

Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu  
665 670 675

Ala Ala Pro Thr Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu  
680 685 690

Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val  
695 700 705

Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala  
710 715 720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His  
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln  
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys  
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly  
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe  
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Asn Ile Gln

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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgtca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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cggtcgacga ccggcccgcg tcatgcggct cctcggtgg tggcaagtat 150  
tgctgtgggt gctggactt cccgtcccg cggtggaggt tgcaaggaa 200  
agtggtcgt tatggtcaga ggagcagcct gctcacccctc tccaggtgg 250  
ggctgtgtac ctgggtgagg aggagctcct gcatgaccgg atgggccagg 300  
acagggcagc agaagaggcc aatgcgggtgc tgggctgga cacccaaggc 350  
gatcacatgg ttagtgcgtc tgtgattcct gggaaagctg aggacaaagt 400  
gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450  
caaggtgcaa cgtccgagag agcctttct ctctggatgg cgctggagca 500  
cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550  
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ccccaaaggt gaactgtgag gagagaaaaca ttacaggatt agaaaatttc 650  
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<211> 360  
<212> PRT  
<213> Homo sapiens

<400> 410  
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Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu  
35 40 45  
  
Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly  
50 55 60  
  
Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala  
65 70 75  
  
Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His  
80 85 90  
  
Met Val Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val  
95 100 105  
  
Ser Ser Glu Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu  
110 115 120  
  
Asp Ser Arg Cys Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly  
125 130 135  
  
Ala Gly Ala His Phe Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu  
140 145 150  
  
Pro Glu Val Ala Glu Ser Asp Ala Ala Pro Thr Glu Asp Ser Asn  
155 160 165  
  
Asn Thr Glu Ser Leu Lys Ser Pro Lys Val Asn Cys Glu Glu Arg  
170 175 180  
  
Asn Ile Thr Gly Leu Glu Asn Phe Thr Leu Lys Ile Leu Asn Met  
185 190 195  
  
Ser Gln Asp Leu Met Asp Phe Leu Asn Pro Asn Gly Ser Asp Cys  
200 205 210  
  
Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys Arg Phe Ser Ala Ser  
215 220 225  
  
Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala Phe Pro Ala Leu  
230 235 240  
  
His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser Leu Ser Thr  
245 250 255  
  
Arg Phe Gly Thr Val Ala Val Pro Asn Ile Leu Leu Phe Gln Gly

	260	265	270
Ala Lys Pro Met Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu			
275	280	285	
Thr Leu Lys Ile Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys			
290	295	300	
Lys Asn Val Val Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro			
305	310	315	
Ser Thr Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu			
320	325	330	
Phe Phe Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu			
335	340	345	
Ser Ile Arg Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu			
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<210> 411			
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<210> 414			
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<212> DNA			
<213> Homo sapiens			

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<400> 414  
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accatttaca agctgaacgg tgtgtccgaa agggacctga agaaatcggt 750  
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<210> 415  
<211> 295  
<212> PRT  
<213> Homo sapiens

<400> 415  
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Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val			
35	40		45
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu			
50	55		60
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln			
65	70		75
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp			
80	85		90
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp			
95	100		105
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln			
110	115		120
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro			
125	130		135
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp			
140	145		150
Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr			
155	160		165
Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp			
170	175		180
Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala			
185	190		195
Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr			
200	205		210
Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn			
215	220		225
Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys			
230	235		240
Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala			
245	250		255
Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile			
260	265		270
Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg			
275	280		285
Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys			

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<220>  
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<400> 417  
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<211> 560  
<212> PRT  
<213> Homo sapiens

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Ala Leu Cys Ala Gln Arg Gly His Arg Thr Tyr Ala Arg Arg Trp  
20 25 30  
  
Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr  
35 40 45  
  
Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp  
50 55 60  
  
Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr  
65 70 75  
  
Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu  
80 85 90  
  
Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu  
95 100 105  
  
Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val  
110 115 120  
  
Gly Thr Gln Asn Pro Phe Ala Phe Leu Met Gly Gly Gln Ser Leu  
125 130 135  
  
Cys Ala Leu Ala Gln Ser Leu Val Ile Phe Ser Pro Ala Lys Leu  
140 145 150  
  
Ala Ala Leu Trp Phe Pro Glu His Gln Arg Ala Thr Ala Asn Met  
155 160 165  
  
Leu Ala Thr Met Ser Asn Pro Leu Gly Val Leu Val Ala Asn Val  
170 175 180  
  
Leu Ser Pro Val Leu Val Lys Gly Glu Asp Ile Pro Leu Met  
185 190 195  
  
Leu Gly Val Tyr Thr Ile Pro Ala Gly Val Val Cys Leu Leu Ser  
200 205 210  
  
Thr Ile Cys Leu Trp Glu Ser Val Pro Pro Thr Pro Pro Ser Ala  
215 220 225  
  
Gly Ala Ala Ser Ser Thr Ser Glu Lys Phe Leu Asp Gly Leu Lys  
230 235 240  
  
Leu Gln Leu Met Trp Asn Lys Ala Tyr Val Ile Leu Ala Val Cys  
245 250 255

Leu Gly Gly Met Ile Gly Ile Ser Ala Ser Phe Ser Ala Leu Leu  
260 265 270

Glu Gln Ile Leu Cys Ala Ser Gly His Ser Ser Gly Phe Ser Gly  
275 . 280 285

Leu Cys Gly Ala Leu Phe Ile Thr Phe Gly Ile Leu Gly Ala Leu  
290 295 300

Ala Leu Gly Pro Tyr Val Asp Arg Thr Lys His Phe Thr Glu Ala  
305 310 315

Thr Lys Ile Gly Leu Cys Leu Phe Ser Leu Ala Cys Val Pro Phe  
320 . 325 330

Ala Leu Val Ser Gln Leu Gln Gly Gln Thr Leu Ala Leu Ala Ala  
335 340 345

Thr Cys Ser Leu Leu Gly Leu Phe Gly Phe Ser Val Gly Pro Val  
350 355 360

Ala Met Glu Leu Ala Val Glu Cys Ser Phe Pro Val Gly Glu Gly  
365 370 375

Ala Ala Thr Gly Met Ile Phe Val Leu Gly Gln Ala Glu Gly Ile  
380 385 390

Leu Ile Met Leu Ala Met Thr Ala Leu Thr Val Arg Arg Ser Glu  
395 400 405

Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp  
410 415 420

Thr Val Ser Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser  
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln  
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly  
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala  
470 475 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg  
485 490 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro  
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr  
515 520 525

Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala  
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Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
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Pro Trp Val Ile Thr  
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<400> 422  
cgggtaata aacctggacg cttgg 25

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<400> 423  
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<210> 424  
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aaaaaaaaaa AAA 4313

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<212> PRT  
<213> Homo sapiens

<400> 425  
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20 25 30

Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val  
35 40 45

Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg  
50 55 60

Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu  
65 70 75

Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg  
80 85 90

Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu  
95 100 105

Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His  
110 115 120

Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe  
125 130 135

Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu  
140 145 150

Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly  
155 160 165

Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe  
170 175 180

Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu  
185 190 195

Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe  
200 205 210

Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser  
215 220 225

Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn  
230 235 240

Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu  
245 250 255

Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp  
260 265 270

Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys  
275 280 285

His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys  
290 295 300

Thr Gly Gln Val Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn  
305 310 315

Pro Ala Tyr Glu Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn  
320 325 330

Pro Ile Pro Ala His Cys Lys Val Leu Ile Lys Val Leu Asp Val  
335 340 345

Asn Asp Asn Ile Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro  
350 355 360

Ser Leu Val Ser Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu  
365 370 375

Val Met Ala Asp Asp Leu Asp Ser Gly His Asn Gly Leu Val His  
380 385 390

Cys Trp Leu Ser Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr  
395 400 405

Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg  
410 415 420

Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln  
425 430 435

Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile  
440 445 450

Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr  
455 460 465

Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile  
470 475 480

Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val  
485 490 495

Ser Tyr Arg Ile Gln Asp Ser Pro Val Ala His Leu Val Ala Ile  
500 505 510

Asp Ser Asn Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr  
515 520 525

Glu Glu Met Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser  
530 535 540

Gly Gln Pro Met Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu  
545 550 555

Leu Asp Ala Asn Asp Asn Ala Pro Glu Val Val Gln Pro Val Leu  
560 565 570

Ser Asp Gly Lys Ala Ser Leu Ser Val Leu Val Asn Ala Ser Thr  
575 580 585

Gly His Leu Leu Val Pro Ile Glu Thr Pro Asn Gly Leu Gly Pro  
590 595 600

Ala Gly Thr Asp Thr Pro Pro Leu Ala Thr His Ser Ser Arg Pro  
605 610 615

Phe Leu Leu Thr Thr Ile Val Ala Arg Asp Ala Asp Ser Gly Ala  
620 625 630

Asn Gly Glu Pro Leu Tyr Ser Ile Arg Asn Gly Asn Glu Ala His  
635 640 645

Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu Phe Val Asn Val  
650 655 660

Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu Leu Glu Ile  
665 670 675

Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg Ala Leu  
680 685 690

Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp Ser  
695 700 705

Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile  
710 715 720

Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu  
725 730 735

Phe Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr  
740 745 750

Asn Cys Arg Glu Ala Glu Ser Thr Tyr Arg Gln Gln Pro Lys Arg  
755 760 765

Pro Gln Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val  
770 775 780

Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His  
785 790 795

Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro  
800 805 810

Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr  
815 820 825

Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu  
830 835 840

Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln  
845 850 855

Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro  
860 865 870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser  
875                        880                        885

Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro  
890                        895                        900

Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His  
905                        910                        915

Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln  
920                        925                        930

Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu  
935                        940                        945

Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln  
950                        955                        960

Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln  
965                        970                        975

Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly  
980                        985                        990

Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg  
995                        1000                        1005

Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp  
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Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu  
1025                        1030                        1035

Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu  
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Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu  
1055                        1060                        1065

Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala  
1070                        1075                        1080

Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala  
1085                        1090                        1095

Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val  
1100                        1105                        1110

Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser  
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Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser  
1130                        1135                        1140

Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala  
1145                        1150                        1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr  
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu  
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

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<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

tgacgttggaa tgcttggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacacctt cagtattgtat gccaaagacag gccaggtcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

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							20		25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
							35		40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
							50		55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Arg	Tyr	Phe	His	Trp	
							65		70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Ile	Leu	Val	Phe	Met	Val	
							80		85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
							95		100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
							110		115					120
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser
							125		130					135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val
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Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly
							155		160					165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn
							170		175					180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln

185	190	195
Thr Met Asp Met Ile Ile Ser Lys Lys	Lys Arg Met Ala Met Ala	
200	205	210
Arg Arg Thr Met Phe Gln Lys Gly Glu	Val His Asn Lys Pro Ser	
215	220	225
Gly Phe Trp Gly Met Ile Lys Ser Val	Thr Thr Ser Ala Ser Gly	
230	235	240
Ser Glu Asn Leu Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu Glu	
245	250	255
Glu Leu Ser Arg Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr Ala	
260	265	270
Thr Lys Glu Arg Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys Tyr	
275	280	285
Phe Asn Phe Leu Gly Tyr Phe Ser Ile	Tyr Cys Val Trp Lys	
290	295	300
Ile Phe Met Ala Thr Ile Asn Ile Val	Phe Asp Arg Val Gly Lys	
305	310	315
Thr Asp Pro Val Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr Leu	
320	325	330
Gly Ile Gln Phe Asp Val Lys Phe Trp	Ser Gln His Ile Ser Phe	
335	340	345
Ile Leu Val Gly Ile Ile Val Thr	Ser Ile Arg Gly Leu Leu	
350	355	360
Ile Thr Leu Thr Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys Ser	
365	370	375
Ser Asn Val Ile Val Leu Leu Ala Gln	Ile Met Gly Met Tyr	
380	385	390
Phe Val Ser Ser Val Leu Leu Ile Arg	Met Ser Met Pro Leu Glu	
395	400	405
Tyr Arg Thr Ile Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe Asn	
410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile	Phe Leu Val Ser Ala Leu	
425	430	435
Ser Ser Ile Leu Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro Glu	
440	445	450
Lys Gln Met Ala Pro		
455		

<211> 407  
<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> 78, 81, 113, 157, 224, 297  
<223> unknown base

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tggctttct tcngcgccaa tgtttaaaga ctatgagata cgtcagtgatg 150  
ttgtacnggt gatcttctcc gtgacgtttgc ccatttcttgc caccatgttt 200  
gagctcatca tctttgaaat cttnnaggta ttgaatagca gctcccgta 250  
ttttcactgg aaaatgaacc tgtgtgtaat tctgctgatc ctggttntca 300  
tggtgccctt ttacattggc tattttatttgc tgagcaatat ccgactactg 350  
cataaacaac gactgctttt ttccctgtctc ttatggctga cctttatgta 400  
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<210> 432  
<211> 457  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434  
<223> unknown base

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tattttttgg atttggggta gnttttttc atgcgcatttgc tgtttaaaga 150  
ctatgagata cgtcagtgatg ttgtacaggt gatnttntcc gtgacgtttgc 200  
cattttcttgc caccatgttttgc gagctcatca ntttgaaat nttaggagta 250  
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tgagcaatat ccgactactg cataaacaac gactgctttt ttccctgtctc 400  
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cattctc 457

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<223> Synthetic oligonucleotide probe

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<210> 434  
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<223> Synthetic oligonucleotide probe

<400> 434  
tcgttgttta tgcagtagtc gg 22

<210> 435  
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<220>  
<223> Synthetic oligonucleotide probe

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attgtttaaa gactatgaga tacgtcagta tgttgtacag g 41

<210> 436  
<211> 3951  
<212> DNA  
<213> Homo sapiens

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<210> 437  
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<213> Homo sapiens

<400> 437  
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Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu  
35 40 45  
Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg  
50 55 60  
Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro  
65 70 75  
Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly  
80 85 90  
Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg  
95 100 105

Val Asp Ile Asp Gln Gly Ala Asp Met Gln Lys Glu Ser Lys Glu  
110 115 120

Asn Gln Trp Leu Gly Val Ser Val Arg Ser Gln Gly Pro Gly Gly  
125 130 135

Lys Ile Val Thr Cys Ala His Arg Tyr Glu Ala Arg Gln Arg Val  
140 145 150

Asp Gln Ile Leu Glu Thr Arg Asp Met Ile Gly Arg Cys Phe Val  
155 160 165

Leu Ser Gln Asp Leu Ala Ile Arg Asp Glu Leu Asp Gly Gly Glu  
170 175 180

Trp Lys Phe Cys Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly  
185 190 195

Phe Cys Gln Gln Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His  
200 205 210

Tyr Leu Leu Phe Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr  
215 220 225

Ala Arg Val Glu Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His  
230 235 240

Leu Asp Asp Gly Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp  
245 250 255

Pro Arg Leu Ile Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser  
260 265 270

Ile Asp Ser Gly Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe  
275 280 285

Val Ala Gly Ala Pro Arg Ala Asn His Lys Gly Ala Val Val Ile  
290 295 300

Leu Arg Lys Asp Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu  
305 310 315

Ser Gly Glu Arg Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val  
320 325 330

Ala Asp Leu Asn Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala  
335 340 345

Pro Tyr Phe Phe Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr  
350 355 360

Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu  
365 370 375

Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala  
380 385 390

Val Leu Gly Asp Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val  
395 400 405

Gly Ala Pro Phe Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly  
410 415 420

Ser Ser Leu Gly Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly  
425 430 435

Glu Ala Val Gly Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser  
440 445 450

Leu Asp Met Asp Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser  
455 460 465

Leu Ala Asp Thr Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His  
470 475 480

Val Ser His Glu Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu  
485 490 495

Gln Pro Asn Cys Ala Gly Gly His Ser Val Cys Val Asp Leu Arg  
500 505 510

Val Cys Phe Ser Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr  
515 520 525

Val Ala Leu Asp Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu  
530 535 540

Arg Gly Gln Val Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu  
545 550 555

Glu Pro Lys His Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln  
560 565 570

His Asp Arg Val Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn  
575 580 585

Val Lys Asp Lys Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser  
590 595 600

Leu Gln Thr Pro Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu  
605 610 615

Pro Pro Val Ala Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln  
620 625 630

Arg Ala Glu Ile His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys  
635 640 645

Ile Cys Gln Ser Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr  
650 655 660

Arg Val Ser Asp Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp  
665 670 675

Gly Thr Thr Ala Leu Phe Ala Leu Ser Gly Gln Pro Val Ile Gly  
680 685 690

Leu Glu Leu Met Val Thr Asn Leu Pro Ser Asp Pro Ala Gln Pro  
695 700 705

Gln Ala Asp Gly Asp Asp Ala His Glu Ala Gln Leu Leu Val Met  
710 715 720

Leu Pro Asp Ser Leu His Tyr Ser Gly Val Arg Ala Leu Asp Pro  
725 730 735

Ala Glu Lys Pro Leu Cys Leu Ser Asn Glu Asn Ala Ser His Val  
740 745 750

Glu Cys Glu Leu Gly Asn Pro Met Lys Arg Gly Ala Gln Val Thr  
755 760 765

Phe Tyr Leu Ile Leu Ser Thr Ser Gly Ile Ser Ile Glu Thr Thr  
770 775 780

Glu Leu Glu Val Glu Leu Leu Ala Thr Ile Ser Glu Gln Glu  
785 790 795

Leu His Pro Val Ser Ala Arg Ala Arg Val Phe Ile Glu Leu Pro  
800 805 810

Leu Ser Ile Ala Gly Met Ala Ile Pro Gln Gln Leu Phe Phe Ser  
815 820 825

Gly Val Val Arg Gly Glu Arg Ala Met Gln Ser Glu Arg Asp Val  
830 835 840

Gly Ser Lys Val Lys Tyr Glu Val Thr Val Ser Asn Gln Gly Gln  
845 850 855

Ser Leu Arg Thr Leu Gly Ser Ala Phe Leu Asn Ile Met Trp Pro  
860 865 870

His Glu Ile Ala Asn Gly Lys Trp Leu Leu Tyr Pro Met Gln Val  
875 880 885

Glu Leu Glu Gly Gly Gln Gly Pro Gly Gln Lys Gly Leu Cys Ser  
890 895 900

Pro Arg Pro Asn Ile Leu His Leu Asp Val Asp Ser Arg Asp Arg  
905 910 915

Arg Arg Arg Glu Leu Glu Pro Pro Glu Gln Gln Glu Pro Gly Glu  
920 925 930

Arg Gln Glu Pro Ser Met Ser Trp Trp Pro Val Ser Ser Ala Glu  
935 940 945

Lys Lys Lys Asn Ile Thr Leu Asp Cys Ala Arg Gly Thr Ala Asn  
950 955 960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala  
965 970 975

Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu  
980 985 990

Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn  
995 1000 1005

Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala  
1010 1015 1020

Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val  
1025 1030 1035

Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu  
1040 1045 1050

Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys  
1055 1060 1065

Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro  
1070 1075 1080

Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe  
1085 1090 1095

Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser  
1100 1105 1110

Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp  
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Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr  
1130 1135 1140

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<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgcctc tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 439  
gctgctgggg actgaatgt agct 24

<210> 440  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 440  
catcctccat gtctccatg aggtcttat tgctccacga agcatac 46

<210> 441  
<211> 1964  
<212> DNA  
<213> Homo sapiens

<400> 441  
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ggagctgcga gcacagtgc ggctcacaac aagatgctca aggtgtcagc 150  
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200  
ccgcggcggt ggctgcagcc gggggcggt cggacggcgg taatttctg 250  
gatgataaac aatggctcac cacaatctc cagtagtaca aggaagtctgg 300  
acagtggAAC aaattccgag acgaagtaga ggatgattat ttccgcactt 350  
ggagtcagg AAAACCCttc gatcaggctt tagatccagc taaggatcca 400  
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tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500  
aagcaggagt agaccatagg cagtgagggtt gtcggatatt atccacactgc 550  
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cccaccagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750  
cagggaaagtg gcaaacagat tgccggactg gttcaaggcc cttcatgaaa 800  
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aattctaagt gaaatttaaa ataaataaat tttaatgac ctgggtctta 1850  
aggattnagg aaaaatatgc atgcttaat tgcatttcca aagtagcatc 1900  
ttgcttagacc tagatgagtc aggataacag agagatacca catgactcca 1950  
aaaaaaaaaa aaaa 1964

<210> 442  
<211> 436  
<212> PRT  
<213> Homo sapiens

<400> 442  
Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp  
1 5 10 15  
Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Gly  
20 25 30  
Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

	35	40	45
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys			
	50	55	60
Phe Arg Asp Glu Val Glu Asp Asp Tyr Phe Arg Thr Trp Ser Pro			
	65	70	75
Gly Lys Pro Phe Asp Gln Ala Leu Asp Pro Ala Lys Asp Pro Cys			
	80	85	90
Leu Lys Met Lys Cys Ser Arg His Lys Val Cys Ile Ala Gln Asp			
	95	100	105
Ser Gln Thr Ala Val Cys Ile Ser His Arg Arg Leu Thr His Arg			
	110	115	120
Met Lys Glu Ala Gly Val Asp His Arg Gln Trp Arg Gly Pro Ile			
	125	130	135
Leu Ser Thr Cys Lys Gln Cys Pro Val Val Tyr Pro Ser Pro Val			
	140	145	150
Cys Gly Ser Asp Gly His Thr Tyr Ser Phe Gln Cys Lys Leu Glu			
	155	160	165
Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser Val Lys Cys Glu			
	170	175	180
Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser Thr Ser Arg			
	185	190	195
Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu Val Ala			
	200	205	210
Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly Ser			
	215	220	225
Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg			
	230	235	240
Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp			
	245	250	255
Met Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln			
	260	265	270
Ser Glu Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr			
	275	280	285
Lys Ala Phe Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile			
	290	295	300
Ser Asn Asn Glu Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro			
	305	310	315
Pro Cys Gln Thr Glu Leu Ser Asn Ile Gln Lys Arg Gln Gly Val			

	320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly			
335	340	345	
Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp			
350	355	360	
Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn			
365	370	375	
Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe			
380	385	390	
Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu			
395	400	405	
Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu			
410	415	420	
Asp Glu Gly Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr			
425	430	435	

Ile

<210> 443  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 443  
cagcaatatt cagaaggcggc aaggg 25

<210> 444  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 444  
catcatggtc atcaccacca tcatcatc 28

<210> 445  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtgtggac agtgctgg 48  
<210> 446  
<211> 3617  
<212> DNA  
<213> Homo sapiens  
  
<400> 446  
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gagcggagac aacagtacct gacgccttt tcagcccg 100  
cagggatggg cgacaagatc tggctgcct tccccgtgt ccttctggcc 150  
gctctgcctc cggtgctgt gcctggggcg gccggctca caccccttc 200  
cgatagcgac ttcacctta cccttcccgc cggccagaag gagtgcttct 250  
accagcccat gcccctgaag gcctcgctgg agatcgagta ccaagttta 300  
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350  
aaccttagtt ttgaacaaa gaaaatcaga tggagttcac actgttagaga 400  
ctgaagttgg tgattacatg ttctgcttt acaatacatt cagcaccatt 450  
tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500  
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatata 550  
tggatatgaa actgaaagac atcctggaat ccatcaacag catcaagtcc 600  
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tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700  
ctatggtaa ttttagtggtc atggtggtgg tgtcagccat tcaagtttat 750  
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caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850  
tggtagtgc aagaccatta atggtcttct ccaaaatatt ttgagatata 900  
aaagttagaa acaggtaaa tttaatgtg aaaattaatg cttcactttc 950  
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tttcctaact ttgaaaaatt ttgcaaatgt cttaggtgt ttaaataat 1100  
gagtattggg cctaattgca acaccagtct gttttaaca ggttctatta 1150  
cccagaactt tttgtaaat gcggcagttt caaattaact gtggaagttt 1200  
tcagtttaa gttataaattc acctgagaat tacctaatttgaat tggattgaat 1250

aaatcttag actacaaaag cccaaacttt ctctattac atatgcac 1300  
ctcctataat gtaaatagaa taatagctt gaaatacaat taggttttg 1350  
agattttat aaccaaatac atttcagtgt aacatattag cagaaagcat 1400  
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tctaaccctt aactaaagtg taggattta aaattaaatg tgaggtaaaa 1600  
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gtagaactat aaataaataat ctagaatctg actggctcat catgacatcc 1900  
tactcataac ataaatcaaa ggagatgatt aatttccagt tagctggaag 1950  
aaactttggc tgttagtttt tattttctac aagaattctg gtttgaatta 2000  
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taaaatggcc tttctgaaca ctttatattt tgatgtgaa gtaaggatta 2150  
gaaacataga ctcccaagtt ttaaacacctt aaatgtgaat aacccatata 2200  
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tcaagtacta gtaatttaac ttcatcatga atgaactata attttaagt 2300  
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gtacaataat gcacaatcag tggctcaa actgctttat acttataaac 3500  
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<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
					35				40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
					50				55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His  
65 70 75

Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys  
80 85 90

Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met  
95 100 105

Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile  
110 115 120

Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu  
125 130 135

Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp  
140 145 150

Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser  
155 160 165

Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe  
170 175 180

Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val  
185 190 195

Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser  
200 205 210

Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg  
215 220 225

Lys Ser Arg Thr

<210> 448  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 448  
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<210> 449  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacgggaaag ggcagccaga tcttgtcgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

ccatccctga gatctttta taaaaaaccc agtcttgct gaccagacaa 50

agcataccag atctcaccag agagtcgcag acactatgct gcctccatg 100

gccctgccc gtgtgtcctg gatgctgctt tcctgcctca ttctcctgtg 150

tcaggttcaa ggtgaagaaa cccagaagga actgccctct ccacggatca 200

gctgtcccaa aggctccaag gcctatggct cccccctgcta tgccttgaaa 250

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ctctggaaaaa ctgggtgtctg tgctcagttgg ggctgaggga tccttcgtgt 350

cctccctgggt gaggagcatt agtaacagct actcatacat ctggattggg 400

ctccatgacc ccacacaggg ctctgagcct gatggagatg gatggagatg 450

gagtagcact gatgtgatga attactttgc atggagaaa aatccctcca 500

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gttcaaggac tagggcaggt gggaaagtca ggcctcagc ttggcgtgca 650

gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700

ttctccccaa actgcctac ctgactacct tgtcatgatc ctccttcittt 750

ttcccttttc ttcacccatca tttcaggctt ttctctgtct tccatgtctt 800

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aaaaaaaaaa 859

<210> 452

<211> 175

<212> PRT

<213> Homo sapiens

<400> 452

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Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln
				20					25					30
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys
						35			40					45
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser
					50				55					60
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys
					65				70					75
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser
					80				85					90
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly
					95				100					105
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp
					110				115					120
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys
					125				130					135
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser
					140				145					150
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala
					155				160					165
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp					
					170				175					

<210> 453

<211> 550

<212> DNA

<213> Homo sapiens

<400> 453

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ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150  
tgcgctgcta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200  
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250  
ccgggagata gtgtacccct tccaggggga ctccacggtg accaagtcc 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcg ccagaccctg 350  
cccggtgcct gctgaatac tgagctgtgc aatgtagacg gggcgccccgc 400  
tctgaacagc ctccactgctg 450  
tccgactgta gagtccccgc ccaccccat gccctatgc ggcccagccc 500  
cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaaaaaaaaa 550  
<210> 454  
<211> 125  
<212> PRT  
<213> Homo sapiens

<400> 454  
Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
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Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
20 25 30  
Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
35 40 45  
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
50 55 60  
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
65 70 75  
Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
80 85 90  
Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
95 100 105  
Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
110 115 120  
Leu Ser Leu Arg Leu  
125

<210> 455  
<211> 1518  
<212> DNA  
<213> Homo sapiens

<400> 455  
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agccgaacct gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100  
attttctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150  
gcgcaagcggg agtacccgg gtcttgcg cgatggtagc ggcggctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctaa 250  
ttccaacgct atcaagaacc tgcccccacc gctgggcggc gctgcggggc 300  
acccaggctc tgcagtcagc gccgcgccgg gaatcctgta cccgggcggg 350  
aataagtacc agaccattga caactaccag ccgtaccgt gcgcagagga 400  
cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgccggaggg 450  
acgcaggcgt gcaaatctgt ctcgcctgca ggaagcgccg aaaacgctgc 500  
atgcgtcacf ctagtgctg ccccgaaat tactgaaaa atgaaatatg 550  
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accacccctt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700  
ttgtctccgg tcatcagact gtgcctcagg attgtgtgt gctagacact 750  
tctggtccaa gatctgtaaa cctgcctgaa aagaaggta agtgtgtacc 800  
aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggta 850  
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ccttcataa ctcataatcata aggtatataca agttctgtgg tttcagttaa 1050  
gcattccaaat aacacccctcc aaaaacctgg agtgcataagag ctttgggttct 1100  
ttatggaaact cccctgtat tgcagtaat tactgtattt taaattctca 1150  
gtgtggact tacctgtaaa tgcaatgaaa ctttaatta tttttctaaa 1200  
ggtgctgcac tgcctatccc tcctcttgc atgtttttt ttgtacacat 1250  
tgattgttat cttgactgac aaatattcta tattgcactg aagtaatca 1300  
tttcagctta tagttcttaa aagcataacc ctttacccca tttaattctca 1350  
gagtctagaa cgcaaggatc tcttggatg acaaattgata ggtacctaaa 1400  
atgttaacatg aaaatactag cttatccctt gaaatgtact atcttaatgc 1450  
ttaaattata ttcccttta ggctgtgata gttttgaaa taaaattaa 1500  
catttaaaaaa aaaaaaaaaa 1518

<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala  
1 5 10 15

Met Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser  
20 25 30

Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu  
35 40 45

Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
50 55 60

Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
65 70 75

Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu  
80 85 90

Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp  
95 100 105

Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg  
110 115 120

Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn  
125 130 135

Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile  
140 145 150

Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu  
155 160 165

Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His  
170 175 180

Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys  
185 190 195

Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys  
200 205 210

Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg  
215 220 225

Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly  
230 235 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser  
245 250 255

Asn Ser Ser Arg Leu His Thr Cys Gln Arg His  
260 265

<210> 457  
<211> 638  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,  
509, 556  
<223> unknown base

<400> 457  
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catttttttt tcttctcct tcnggagtcc ttntgagang atggtttgg 150  
gcgcagcggg agctaaccgg gtttttgtn gcgtggtag cggcggttt 200  
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acccaggntt tgcagtcagc gccgcgcgg gaatcctgta cccgggggg 350  
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cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgccggagggg 450  
angcgggcgt gcaaantgt ntngcctgca ggaagcgcgg aaaacgctgc 500  
atgcgtcang ctatgtctg ccccgaaat tactgaaaa atgaaatatg 550  
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ctgaaagctt tggtaatgat catagcacct tggatgg 638

<210> 458  
<211> 4040  
<212> DNA  
<213> Homo sapiens

<400> 458  
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ttctctcctg cacgcgggtgc ttgggctcgg ccaggcgggg tccgccgcca 150  
gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200  
gtatattttt gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250  
ttcacagatt aatattttt gggacagatt tgtgatgctt gattcaccc 300



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<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
					20				25				30	

Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
					35				40				45	

Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
					50				55				60	

Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
					65				70				75	

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu  
80 85 90

Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu  
95 100 105

Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr  
110 115 120

Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu  
125 130 135

Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe  
140 145 150

Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala  
155 160 165

Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg  
170 175 180

Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met  
185 190 195

Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly  
200 205 210

Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu  
215 220 225

Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu  
230 235 240

Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala  
245 250 255

Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys  
260 265 270

Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu  
275 280 285

Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn  
290 295 300

Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg  
305 310 315

Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn  
320 325 330

Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu  
335 340 345

Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala  
350 355 360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala  
365 370 375

Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly  
380 385 390

Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val  
395 400 405

Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn  
410 415 420

Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro  
425 430 435

Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu  
440 445 450

Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His  
455 460 465

Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr  
470 475 480

Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His  
485 490 495

Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro  
500 505 510

Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr  
515 520 525

Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro  
530 535 540

Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met  
545 550 555

Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys  
560 565 570

Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr  
575 580 585

Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln  
590 595 600

Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg  
605 610 615

Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr  
620 625 630

Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp  
635 640 645

Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe  
650 655 660

Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val  
665 670 675

Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln  
680 685 690

Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr  
695 700 705

Glu Arg Ala Lys Arg Asn Phe Gln Glu Gln Ile Asn Thr Arg  
710 715 720

Asp Ala Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr  
725 730 735

Leu Arg Asn Gln Gly Lys Arg Asn Lys Asp Glu Leu  
740 745

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

actccccagg ctgttcacac tgcc 24

<210> 461

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

gatcagccag ccaataccag cagc 24

<210> 462

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

gtgggtatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463

<211> 1818

<212> DNA

<213> Homo sapiens

<400> 463

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caccatcatc tactcctact tggagtcgtt ggtgaagttt ttcattcctc 150  
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200  
catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat 250  
attggttctg tgggatatta ataagcgcgg tgtggagaa actgcagctg 300  
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<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

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Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly  
35 40 45

His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln  
50 55 60

Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu  
65 70 75

Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr  
80 85 90

Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn  
95 100 105

Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn  
110 115 120

Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu  
125 130 135

Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp  
140 145 150

Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly

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His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro			
170	175		180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe			
185	190		195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly			
200	205		210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe			
215	220		225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp			
230	235		240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys			
245	250		255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln			
260	265		270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln			
275	280		285
Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys			
290	295		300
<210> 465			
<211> 1547			
<212> DNA			
<213> Homo sapiens			
<400> 465			
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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
								20		25				30

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
								35		40				45

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
								50		55				60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser  
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln  
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp  
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln  
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser  
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro  
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala  
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg  
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro  
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala  
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys  
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys  
230 235 240

Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe  
245 250 255

Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe  
260 265 270

Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro  
275 280 285

Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe  
290 295 300

Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu  
305 310 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His  
320 325 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu  
335 340 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
350 355 360  
Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
365 370 375  
Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
380 385 390  
Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
395 400 405  
Pro Lys Pro Glu Asn Leu Leu Arg Asp  
410

<210> 467  
<211> 1071  
<212> DNA  
<213> Homo sapiens

<400> 467  
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ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100  
acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150  
gggggcgggc gcggcatcg agctgggatc gtgcgcgcct tcgtgaacag 200  
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cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600  
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ctccgaagcc aacttctgca cggcattga actgctcgtg acgggggtg 850  
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cccgatatcc cttcctgatt tctctcattt ctacttgggg cccccttcct 950  
aggactctcc caccccaaac tccaacctgt atcagatgca gcccccaagc 1000  
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<210> 468

<211> 270

<212> PRT

<213> Homo sapiens

<400> 468

Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr  
1 5 10 15

Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val  
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Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly  
35 40 45

Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu  
50 55 60

Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu  
65 70 75

Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala  
80 85 90

Gly His His Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln  
95 100 105

Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr  
110 115 120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn  
125 130 135

Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln  
140 145 150

Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr  
155 160 165

Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn  
170 175 180

Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu  
185 190 195

Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met  
200 205 210

Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly  
215 220 225

Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly  
230 235 240

Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys  
245 250 255

Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser  
260 265 270

<210> 469

<211> 687

<212> DNA

<213> Homo sapiens

<400> 469

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ccagccccagg agccccaaaa gcaagagggaa ggggcaaggg cggcctggc 150  
ccctggccccc tggccctcac caggtgccac tggacctggc gtcacggatg 200  
aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatgg 250  
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gaccatcgct gtgggctgca cctgcacatt ctgaatcacc tggcccagaa 600  
gccaggccag cagcccgaga ccatcctct tgcacctttg tgccaagaaa 650  
ggcctatgaa aagtaaacac tgactttga aagcaag 687

<210> 470

<211> 180

<212> PRT

<213> Homo sapiens

<400> 470

Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile  
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Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
20 25 30

Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val  
35 . 40 45

Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu  
50 55 60

Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn  
65 70 75

Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu  
80 85 90

Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile  
95 100 105

Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg  
110 115 120

Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp  
125 130 135

Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg  
140 145 150

Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln  
155 160 165

Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe  
170 175 180

<210> 471  
<211> 2368  
<212> DNA  
<213> Homo sapiens

<400> 471  
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cgcccccgca gtaacggcgc tcctggccgc ctggatcgcg gctgtggcg 200  
cgacggcagg ccccgaggag gccgcgtgc cgccggagca gagccgggtc 250  
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aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450  
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gatttcctt cagtatgtg cttttggta aagaattaat gaactccagt 2250  
acctgaaagt gaaagatttgc attttggttc catttctgt aatcttccaa 2300  
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agggaggcta atttcttt 2368

<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala  
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20 25 30

Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser  
35 40 45

Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
50 55 60

Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
65 70 75

Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
80 85 90

Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val  
95 100 105

Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg  
110 115 120

Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile  
125 130 135

Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys  
140 145 150

Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser  
155 160 165

Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr  
170 175 180

Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala  
185 190 195

Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile  
200 205 210

Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg  
215 220 225

Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln  
230 235 240

Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu  
245 250 255

Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu  
260 265 270

Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Asp Asn Leu  
275 280 285

Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly  
290 295 300

Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu  
305 310 315

Glu Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr  
320 325 330

Glu Val Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala  
335 340 345

Asp Lys Gly Leu

<210> 473  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 473  
gtccagccca tgaccgcctc caac 24

<210> 474  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctcctcat ccacaccaggc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

tgggatgctg aaattttacg ccccatggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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gcccacatga tttgacttag agattcttt ttgtccacag acagtcatct 100

caggggcaga aagaaaagag ctcccaaatg ctatatctat tcaggggctc 150

tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200

atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250

tttcagagaa aggatcggtgt gctgcatttc tccttggcg cctcattgtct 300

gtaattttgg gaatcctatg ctggtaata ctggtgatag ctgtggcct 350

gggtaccatg ggggttcttt ccagcccttg tcctcctaattt tggatttat 400

atgagaagag ctgttatcta ttcagcatgt cactaaattc ctggatgg 450

agtaaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500

ctcaaattgaa ttgggattta tagaaaaaca agtgcattcc caacctgata 550

attcatttttgc gataggcattt tctcgcccccc agactgaggt accatggctc 600

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aagttttcaaa tgtaagagga agggtggaga aggagagaga aatatgtgag 800

gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgaggtca 850

agataaaatgc agaaaatgtt tagagagctt ggccaactgt aatcttaacc 900

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<210> 477  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 477  
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Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu  
35 40 45  
  
Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile  
50 55 60  
  
Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro  
65 70 75  
  
Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met  
80 85 90  
  
Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu  
95 100 105  
  
Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe  
110 115 120  
  
Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile  
125 130 135  
  
Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp  
140 145 150  
  
Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala  
155 160 165  
  
Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser  
170 175 180  
  
Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys  
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Glu Lys Lys Phe Ser Met  
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<210> 478

<211> 27  
<212> DNA  
<213> Artificial Sequence

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<400> 478  
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<210> 479  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 479  
acaagtgtct tcccaacctg 20

<210> 480  
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<220>  
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<400> 480  
atcctccag agccatggta cctc 24

<210> 481  
<211> 51  
<212> DNA  
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<220>  
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<400> 481  
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<210> 482  
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<212> DNA  
<213> Homo sapiens

<400> 482  
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tcttggctca tcgtaacctc cacctcccg gttcaagtga ttctcatgcc 150

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<210> 483  
<211> 693  
<212> PRT  
<213> Homo sapiens

<400> 483  
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Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser  
35 40 45  
Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn  
50 55 60  
Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His  
65 70 75  
Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe  
80 85 90

Cys Leu Tyr Trp Asn Arg His Ala Gly Arg Leu His Leu Leu Tyr  
95 100 105

Gly Lys Arg Asp Phe Leu Leu Ser Asp Lys Ala Ser Ser Leu Leu  
110 115 120

Cys Phe Gln His Gln Glu Glu Ser Leu Ala Gln Gly Pro Pro Leu  
125 130 135

Leu Ala Thr Ser Val Thr Ser Trp Trp Ser Pro Gln Asn Ile Ser  
140 145 150

Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser Phe His Ser Pro Pro  
155 160 165

His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys  
170 175 180

Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys  
185 190 195

Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln  
200 205 210

Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met  
215 220 225

Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu  
230 235 240

Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln  
245 250 255

Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro  
260 265 270

Arg Thr Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu  
275 280 285

Lys Arg Leu Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln  
290 295 300

Asp Lys Asn Ser Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile  
305 310 315

Val Val Gln Asn Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val  
320 325 330

Leu Thr Phe Gln His Gln Leu Gln Pro Lys Asn Val Thr Leu Gln  
335 340 345

Cys Val Phe Trp Val Glu Asp Pro Thr Leu Ser Ser Pro Gly His  
350 355 360

Trp Ser Ser Ala Gly Cys Glu Thr Val Arg Arg Glu Thr Gln Thr  
365 370 375

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val  
380 385 390

Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu  
395 400 405

Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val  
410 415 420

Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg  
425 430 435

Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu  
440 445 450

Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro  
455 460 465

Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile  
470 475 480

Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu  
485 490 495

Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr  
500 505 510

Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly  
515 520 525

Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp  
530 535 540

Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly  
545 550 555

Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser  
560 565 570

Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn  
575 580 585

Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg  
590 595 600

Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu  
605 610 615

Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe  
620 625 630

Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile  
635 640 645

Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser  
650 655 660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn  
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

<210> 484

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 68, 70, 84, 147

<223> unknown base

<400> 484

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cggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200

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tttctgttca acatgg 516

<210> 485

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

ggcattggag cagtgtggg tg 22

<210> 486

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

tggaggccta gatgcggctg gacg 24

<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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aagagggctc tagaaaaaaag ttttggatgg gattatgtgg aaactaccct 150

gcgattctct gctgccagag caggctcgcc gcttccaccc cagtgcagcc 200

ttcccctggc ggtggtaaaa gagactcggg agtcgtgct tccaaagtgc 250

ccgcccgtgag tgagctctca ccccagtca ccaaattgagc ctcttcgggc 300

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gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400

cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450

gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggc 500

ttggtatgga gattagtagc agtagagggaa aatgtatgga tacaacttac 550

gtttgatgaa agatttggc ttgaagaccc agaagatgac atatgcaagt 600

atgattttgt agaagttgag gaacccagtg atggaactat attagggcgc 650

tggtggtt ctggtaactgt accagggaaa cagatttcta aaggaaatca 700

aattaggata agatttgtat ctgatgaata ttttcctct gaaccaggg 750

tctgcatcca ctacaacatt gtcatgccac aattcacaga agctgtgagt 800

ccttcagtgc taccccttc agctttgcca ctggacctgc ttaataatgc 850

tataactgcc ttttagtacct tggaaagacct tattcgatat cttgaaccag 900

agagatggca gttggactta gaagatctat ataggccaac ttggcaactt 950

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

Met Ser Leu Phe Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly  
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Gln Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe  
20 25 30

Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln  
35 40 45

His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser  
50 55 60

Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp  
65 70 75

Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe  
80 85 90

Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys  
95 100 105

Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu  
110 115 120

Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser  
125 130 135

Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe  
140 145 150

Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro  
155 160 165

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala  
170 175 180

Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr  
185 190 195

Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu  
200 205 210

Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys  
215 220 225

Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu  
230 235 240

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe  
245 250 255

Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe  
260 265 270

Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala  
275 280 285

Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys  
290 295 300

Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr  
305 310 315

Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu  
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His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly  
335 340 345

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 490

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<400> 491  
caccacagcg tttaaccagg 20  
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acaacaggca cagttccac 20  
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<210> 495  
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<212> DNA  
<213> Homo sapiens

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ggacactgaa gagacaatt cttatcctt ttaacataat cctaattcc 150

aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200  
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acaactgcct agttaccaa ggagaggcct ggc 3283

<210> 496  
<211> 1049  
<212> PRT  
<213> Homo sapiens

<400> 496  
Met Val Phe Pro Met Trp Thr Leu Lys Arg Gln Ile Leu Ile Leu  
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Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn  
35 40 45  
His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro  
50 55 60  
Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
65 70 75  
His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
80 85 90  
Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu  
95 100 105  
Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
110 115 120  
Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp  
125 130 135  
Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
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Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
155 160 165  
Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
170 175 180  
Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile  
185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser  
200 205 210  
Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser  
215 220 225  
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile  
230 235 240  
Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp  
245 250 255  
Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys  
260 265 270  
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala  
275 280 285  
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn  
290 295 300  
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys  
305 310 315  
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile  
320 325 330  
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu  
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Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met  
350 355 360  
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu  
365 370 375  
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu  
380 385 390  
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly  
395 400 405  
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe  
410 415 420  
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro  
425 430 435  
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr  
440 445 450  
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr  
455 460 465  
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys  
470 475 480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly  
485 490 495

Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser  
500 505 510

Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser  
515 520 525

Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro  
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Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp  
545 550 555

Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val  
560 565 570

Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile  
575 580 585

Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys  
590 595 600

Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr  
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Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His  
620 625 630

Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu  
635 640 645

Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn  
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Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro  
665 670 675

Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe  
680 685 690

Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp  
695 700 705

Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn  
710 715 720

Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile  
725 730 735

Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg  
740 745 750

Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr  
755 760 765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu  
770 775 780

His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val  
785 790 795

Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr  
800 805 810

Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val  
815 820 825

Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu  
830 835 840

Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val  
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Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile  
860 865 870

Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile  
875 880 885

Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys  
890 895 900

Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys  
905 910 915

Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu  
920 925 930

Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln  
935 940 945

Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys  
950 955 960

Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His  
965 970 975

Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe  
980 985 990

Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys  
995 1000 1005

Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln  
1010 1015 1020

Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr  
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<212> DNA  
<213> *Homo sapiens*

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<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val  
35 40 45

Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr  
50 55 60

Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile  
65 70 75

Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu Thr  
80 85 90

Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly  
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Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala  
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Phe Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn  
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Gln Leu Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu  
140 145 150

Leu Ser Leu Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly  
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Ile Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn  
170 175 180

Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly  
185 190 195

Val Phe Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe  
200 205 210

Asn Ser Leu Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg  
215 220 225

Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu  
230 235 240

Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly  
245 250 255

Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys  
260 265 270

Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn  
275 280 285

Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg  
290 295 300

Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val  
305 310 315

Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly  
320 325 330

Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser  
335 340 345

Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser  
350 355 360

Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg  
365 370 375

Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu  
380 385 390

Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe  
395 400 405

Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu  
410 415 420

Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys  
425 430 435

Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His  
440 445 450

Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser  
455 460 465

Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala  
470 475 480

Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe  
485 490 495

Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu  
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Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu  
515 520 525

Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn  
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Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp  
545 550 555

Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile  
560 565 570

Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn  
575 580 585

Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr  
590 595 600

Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe  
605 610 615

Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg  
620 625 630

Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp  
635 640 645

Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu  
650 655 660

Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met  
665 670 675

Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu  
680 685 690

Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp  
695 700 705

Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser  
710 715 720

His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val  
725 730 735

Ser Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr  
740 745 750

Ile Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr Lys Leu Ser  
755 760 765

Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile  
770 775 780

Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile  
785 790 795

Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg  
800 805 810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp  
815 820 825

Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr  
830 835 840

Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp  
845 850 855

Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr  
860 865 870

Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser  
875 880 885

Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu  
890 895 900

Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu  
905 910 915

Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp  
920 925 930

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val  
935 940 945

Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe  
950 955 960

Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile  
965 970 975

Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu  
980 985 990

Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro  
995 1000 1005

Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn  
1010 1015 1020

Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val  
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Asp Ser Ile Lys Gln Tyr  
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 505  
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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 506

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Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu

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Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala			
185		190	195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu			
200		205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala			
215		220	225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu			
230		235	240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu			
245		250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys			
260		265	270
Lys Asp Ser			

<210> 507  
<211> 1700  
<212> DNA  
<213> Homo sapiens

<400> 507  
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tggcagcaaa gttcagcttg gctgggcccgttgtgagggg cttcgcgcta 200  
cgccctgcgg tgtcccgagg gctgaggtct cctcatcttc tccctagcag 250  
tggatgagca acccaacggg ggccccggga gggaaactgg ccccgaggg 300  
gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350  
gcagccccc ggaccgggg ggcacaggtg gccccacca cccggaggag 400  
cagctcctgc ccctgtccgg gggatgactg attctcctcc gccaggccac 450  
ccagaggaga aggccacccc gcctggaggc acaggccatg aggggctctc 500  
aggaggtgct gctgatgtgg cttctggtgt tggcagtggg cggcacagag 550  
cacgcctacc ggccccggcg tagggtgtgt gctgtccggg ctcacggg 600  
ccctgtctcc gagtcgttgc tgcaagcgtgt gtaccagccc ttcctcacca 650

cctgcgacgg gcaccgggcc tgcagcacct accgaaccat ctataggacc 700  
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caatatgccca gccgcccattgc cggAACGGAG ggagctgtgt ccagcctggc 850  
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cggggtgact gagcggaaagg ccaggcaggg ctttccttcc cttccttc 1450  
cctttcctcg ggaggctccc cagaccctgg catggatgg gctggatct 1500  
tctctgtgaa tccaccctg gctaccccca ccctggctac cccaacggca 1550  
tcccaaggcc aggtggaccc tcagctgagg gaaggtacga gtcctctgct 1600  
ggagcctggg acccatggca caggccaggc agcccgagg ctgggtgggg 1650  
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
					20				25				30	

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
						35			40				45	

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
                   50                      55                      60  
  
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
                   65                      70                      75  
  
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
                   80                      85                      90  
  
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
                   95                      100                    105  
  
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
                   110                      115                    120  
  
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
                   125                      130                    135  
  
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
                   140                      145                    150  
  
 Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
                   155                      160                    165  
  
 Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
                   170                      175                    180  
  
 Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
                   185                      190                    195  
  
 Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
                   200                      205                    210  
  
 Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
                   215                      220                    225  
  
 Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
                   230                      235                    240  
  
 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
                   245                      250                    255  
  
 Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
                   260                      265                    270  
  
 Lys Asp Ser

<210> 509  
 <211> 1538  
 <212> DNA  
 <213> Homo sapiens

<400> 509  
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gcggccacca tggccacgcc tgggctccag cagcatcagc agccccagg 200  
accggggagg cacaggtggc ccccaccacc cgaggagca gctcctgcc 250  
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gccaccccgc ctggaggcac aggccatgag gggctctcg gaggtgctgc 350  
tgatgtggct tctgggttg gcagtggcg gcacagagca cgcctaccgg 400  
cccgccgta gggtgtgtgc tgtccggct cacgggacc ctgtctccga 450  
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accgggcctg cagcacctac cgaaccatct ataggaccgc ctaccggcg 550  
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cctgcaggat ggcggggtga cacttgccag tcagatgtgg atgaatgcag 750  
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cacccctggc taccggacc ctggctaccc caacggcatc ccaaggccag 1400  
gtggggccctc agctgaggga aggtacgagc tccctgctgg agcctgggac 1450  
ccatggcaca ggccaggcag cccggaggct gggtggggcc tcagtgggg 1500

ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
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Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150

Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
260 265 270

Lys Asp Ser

<210> 511  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 511  
tggagcagca atatgccagc c 21

<210> 512  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 512  
ttttccactc ctgtcgggtt gg 22

<210> 513  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 513  
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514  
<211> 2690  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2039-2065  
<223> unknown base

<400> 514  
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ggagacagcc tcccgccccg gggaggacaa gtcgctgcca ccttggctg 100

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agtgggtct ccgtttca ggccggctcc cccttcctgg tctcccttct 200  
cccgctgggc cggttatcg ggaggagatt gtctccagg gctagcaatt 250  
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atggccgcgt catgatggcc cggcaaaagg gcatttcta cctgaccctt 500  
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caactgtgtg gagcgcttcg accatcaactg cccctgggtg gggatttgt 900  
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ttctagaagt cctcatttgc ttcttacac tctggccgt cgtggactg 1100  
actggatttc atacttcct cgtggctctc aaccagacaa ccaatgaaga 1150  
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cccaagtgc tggatcgaag gggatatttg ccactggagg aaagtggaaag 1300  
tcgacctccc agtactcaag agaccagtag cagccttgc ccacagagcc 1350  
cagccccac agaacacactg aactcaaatg agatgccggaa ggacagcagc 1400  
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caccggcaga gtcccagagc cacttcaccc tgggggtggg ctgtggcccc 2500  
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ccagggtcct gtctggatga cttatgcgggtt gggggagtgt aaaccggAAC 2650  
ttttcatcta tttgaaggcg attaaactgt gtctaatgca 2690

<210> 515  
<211> 364  
<212> PRT  
<213> Homo sapiens

<400> 515  
Met Ser Val Met Val Val Arg Lys Lys Val Thr Arg Lys Trp Glu  
1 5 10 15

Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met

20	25	30
Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile		
35	40	45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu		
50	55	60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu		
65	70	75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp		
80	85	90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile		
95	100	105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln		
110	115	120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile		
125	130	135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro		
140	145	150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe		
155	160	165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn		
170	175	180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr		
185	190	195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser		
200	205	210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr		
215	220	225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val		
230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		

305 310 315

Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu  
320 325 330

His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu  
335 340 345

Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala  
350 355 360

Glu Ala Glu Lys

<210> 516

<211> 255

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 38, 88, 118, 135, 193, 213, 222

<223> unknown base

<400> 516

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ccccctgggtg ggaaattgtg ttggaaagag gaactaccgc tanttctacc 200

tcttcatcct ttntctctcc cncctcacaa tctatgtctt cgccctcaac 250

atcgt 255

<210> 517

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgatc aagaatttcc 20  
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<212> DNA  
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<223> Synthetic oligonucleotide probe  
  
<400> 519  
agtggaaagtc gacctccc 18  
  
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<223> Synthetic oligonucleotide probe  
  
<400> 520  
ctcacctgaa atctctcata gccc 24  
  
<210> 521  
<211> 50  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 521  
cgcaaaaccc attttggag caggaattcc aatcatgtct gtgatggtgg 50  
  
<210> 522  
<211> 1679  
<212> DNA  
<213> Homo sapiens  
  
<400> 522  
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caaaaaagaa gaaaaagaag aaaaaaaaaa atcatgaaaa ccatccagcc 150  
aaaaatgcac aattcttatct cttggcaat ctgcacgggg ctggctgctc 200  
tgtgtctctt ccaaggagtg cccgtgcga gcggagatgc cacccccc 250  
aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300  
gtgcactatt gacaaccggg tcacccgggt ggctggcta aaccgcagca 350  
ccatccctcta tgctggaaat gacaagtggt gcctggatcc tcgcgtggtc 400

cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450  
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caaagacctc tagggcac ctcattgtgc aagtatctcc caaaattgta 550  
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gccgccacca ccaccaccaa cacaacagca atggcaacac cgacagcaac 1250  
caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300  
gaaatttgag ggagggaaac aaagaatact ttgggggaa aagagttta 1350  
aaaaagaaat tgaaaattgc cttgcagata tttaggtaca atggagttt 1400  
ctttcccaa acgggaagaa cacagcacac ccggcttggc cccactgca 1450  
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tctgcccaca gagtgcccc acgtggaaca ttctggagct ggccatccca 1550  
aattcaatca gtccatagag acgaacagaa tgagaccttc cggccaaagc 1600  
gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttgg 1650  
aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp Ala			
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Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro			
20	25	30	
Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val			
35	40	45	
Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp			
50	55	60	
Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu			
65	70	75	
Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu			
80	85	90	
Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val			
95	100	105	
Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp			
110	115	120	
Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser			
125	130	135	
Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly			
140	145	150	
Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro			
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Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro			
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Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile			
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Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr			
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Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp			
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Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys			
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Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala  
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Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp  
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Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu  
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Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp  
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Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro  
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50 55 60  
Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile  
65 70 75  
Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser  
80 85 90  
Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn  
95 100 105  
Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr

110 115 120

Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val  
125 130 135

Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu  
140 145 150

Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu  
155 160 165

Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe  
170 175 180

Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln  
185 190 195

Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro  
200 205 210

Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile  
215 220 225

Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu  
230 235 240

Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe Glu Trp  
245 250 255

Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile  
260 265 270

Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val  
275 280 285

Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys  
290 295 300

Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr  
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Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys  
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Leu Lys Asn Ala Ile Leu Gln  
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<212> DNA

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cctgatcctg ctcaccgctg gcgcgtggct gctgggtggc caagttctga 300  
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tggagaacac ctggctcagg gtgcattcgag gctgcaagtc ctgcaggccc 450  
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gtgccaaggg tgagcctggc agtgcgtggc cccctggcg agcaggactt 1100  
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cccaagggag cccctggaca agctggccag aaggagacc agggagtgaa 1300  
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aaaactcagt gtccgtcagg attgtcgca gtagtaaccg aggccggct 1400  
gaagtttact acagtggtaac ctgggggaca atttgcgtatg acgagtggca 1450

aattctgat gccattgtct tctgcccat gctgggttac tccaaaggaa 1500  
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gttcagtgtc gggcacgga gagtaccctg tggagctgca ccaagaatag 1600  
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<210> 614  
<211> 520  
<212> PRT  
<213> Homo Sapien

<400> 614  
Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu  
1 5 10 15  
Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu  
20 25 30  
Ile Asn Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser  
35 40 45  
Leu Ala Val Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala  
50 55 60  
Gly Leu Leu Val Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg  
65 70 75  
Val Leu Glu Met Tyr Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp  
80 85 90  
Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His Pro Gly Glu His  
95 100 105  
Leu Ala Gln Gly Ala Ser Arg Leu Gln Val Leu Gln Ala Gln Leu  
110 115 120  
Thr Trp Val Arg Val Ser His Glu His Leu Leu Gln Arg Val Asp  
125 130 135  
Asn Phe Thr Gln Asn Pro Gly Met Phe Arg Ile Lys Gly Glu Gln  
140 145 150  
Gly Ala Pro Gly Leu Gln Gly His Lys Gly Ala Met Gly Met Pro  
155 160 165  
Gly Ala Pro Gly Pro Pro Gly Pro Pro Ala Glu Lys Gly Ala Lys  
170 175 180  
Gly Ala Met Gly Arg Asp Gly Ala Thr Gly Pro Ser Gly Pro Gln

	185	190	195
Gly Pro Pro Gly Val Lys Gly Glu Ala Gly Leu Gln Gly Pro Gln			
200	205		210
Gly Ala Pro Gly Lys Gln Gly Ala Thr Gly Thr Pro Gly Pro Gln			
215	220		225
Gly Glu Lys Gly Ser Lys Gly Asp Gly Gly Leu Ile Gly Pro Lys			
230	235		240
Gly Glu Thr Gly Thr Lys Gly Glu Lys Gly Asp Leu Gly Leu Pro			
245	250		255
Gly Ser Lys Gly Asp Arg Gly Met Lys Gly Asp Ala Gly Val Met			
260	265		270
Gly Pro Pro Gly Ala Gln Gly Ser Lys Gly Asp Phe Gly Arg Pro			
275	280		285
Gly Pro Pro Gly Leu Ala Gly Phe Pro Gly Ala Lys Gly Asp Gln			
290	295		300
Gly Gln Pro Gly Leu Gln Gly Val Pro Gly Pro Pro Gly Ala Val			
305	310		315
Gly His Pro Gly Ala Lys Gly Glu Pro Gly Ser Ala Gly Ser Pro			
320	325		330
Gly Arg Ala Gly Leu Pro Gly Ser Pro Gly Ser Pro Gly Ala Thr			
335	340		345
Gly Leu Lys Gly Ser Lys Gly Asp Thr Gly Leu Gln Gly Gln Gln			
350	355		360
Gly Arg Lys Gly Glu Ser Gly Val Pro Gly Pro Ala Gly Val Lys			
365	370		375
Gly Glu Gln Gly Ser Pro Gly Leu Ala Gly Pro Lys Gly Ala Pro			
380	385		390
Gly Gln Ala Gly Gln Lys Gly Asp Gln Gly Val Lys Gly Ser Ser			
395	400		405
Gly Glu Gln Gly Val Lys Gly Glu Lys Gly Glu Arg Gly Glu Asn			
410	415		420
Ser Val Ser Val Arg Ile Val Gly Ser Ser Asn Arg Gly Arg Ala			
425	430		435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly Thr Ile Cys Asp Asp Glu			
440	445		450
Trp Gln Asn Ser Asp Ala Ile Val Phe Cys Arg Met Leu Gly Tyr			
455	460		465
Ser Lys Gly Arg Ala Leu Tyr Lys Val Gly Ala Gly Thr Gly Gln			

470 475 480

Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu  
485 490 495

Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His  
500 505 510

Glu Glu Asp Ala Gly Val Glu Cys Ser Val  
515 520

<210> 615

<211> 647

<212> DNA

<213> Homo Sapien

<400> 615

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attnaagaag catcctctgc caagacccaa aggaaagaag aaaaaggccc 150  
aaaagccaaa atgaaactga tggtaacttgt tttcaccatt gggctaactt 200  
tgctgctagg agttcaagcc atgcctgcaa atgcctctc ttgctacaga 250  
aagataactaa aagatcacaa ctgtcacaac cttccggaag gagtagctga 300  
cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350  
gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgccc 400  
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tcaatgagaa tcttcatgtt ttctggagaa caccatttctt gatttcccc 500  
aaactgcact acatcagttt aactgcattt ctagttctta tatagtgcaa 550  
tagagcatag attctataaa ttcttacttg tctaagacaa gtaaatctgt 600  
gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaaa 647

<210> 616

<211> 98

<212> PRT

<213> Homo Sapien

<400> 616

Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu  
1 5 10 15

Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg  
20 25 30

Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val  
35 40 45

Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp  
50 55 60

Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu  
65 70 75

Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser  
80 85 90

Phe Val Ile Pro Cys Asn Asn Gln  
95

<210> 617

<211> 2558

<212> DNA

<213> Homo Sapien

<400> 617

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cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100

accccgccgt ggtggttgga gggcgccag tagagcagca gcacaggcgc 150

gggtccccggg aggccggctc tgctcgccgag gagatgtgga atctccttca 200

cgaaccgcac tcggctgtgg ccaccgcgcg ccgcggcgc tggctgtgcg 250

ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg ctccctcttc 300

gggtggttta taaaatcctc caatgaagct actaacatta ctccaaagca 350

taatatgaaa gcattttgg atgaattgaa agctgagaac atcaagaagt 400

tcttacataa ttttacacag ataccacatt tagcaggaac agaacaac 450

tttcagcttg caaagcaaattcaatcccag tggaaagaat ttggcctgga 500

ttctgtttag ctagtcatt atgatgtcct gttgtcctac ccaaataaga 550

ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagatttc 600

aacacatcat tatttgaacc acctcctcca gatatgaaa atgttcgg 650

tattgtacca ctttcagtg ctttctctcc tcaaggaatg ccagagggcg 700

atcttagtgta tgttaactat gcacgaactg aagacttctt taaattggaa 750

cgggacatga aaatcaatttgcctggaaa attgtatgg ccagatatgg 800

gaaagtttc agaggaaata aggtaaaaa tgcccagctg gcagggccca 850

aaggagtcat tctctactcc gaccctgctg actacttgc tcctgggtg 900

aagtcctatc cagacggttg gaatcttccctt ggaggtggtg tccagcgtgg 950

aaatatccta aatctgaatg gtgcaggaga ccctctcaca ccaggttacc 1000  
cagcaaatga atatgcttat aggcggtggaa ttgcagaggc tgggtgttt 1050  
ccaagtattc ctgttcatcc aattggatac tatgtatgcac agaagctcct 1100  
agaaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150  
tcaaagtgcc ctacaatgtt ggacctggct ttactggaaa ctttctaca 1200  
caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250  
caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300  
ttctgggagg tcaccggac tcatgggtgt ttgggtgtat tgaccctcag 1350  
agtggagcag ctgttgtca taaaatttg aggagcttg gaacactgaa 1400  
aaaggaaggg tggagaccta gaagaacaat tttgtttgca agctggatg 1450  
cagaagaatt tggcttctt gttctactg agtgggcaga ggagaattca 1500  
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agaaggaaac tacactctga gagttgattt tacaccgctg atgtacagct 1600  
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aattgggaaa caaacaattt cagcggctat ccactgtatc acagtgtcta 1850  
tgaaacatat gagttggggaaaat tggatccatg tttaaatatc 1900  
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acagaaattt cttccaagtt cagtgagaga ctccaggact ttgacaaaag 2150  
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gagcatttat tggatccatg gggttaccag acaggcctt ttataggcat 2250  
gtcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300  
aggaattttat gatgctctgt ttgatattga aagcaaagtg gacccttcca 2350  
aggcctgggg agaagtgaag agacagattt atgttgcagc cttcacagtg 2400

caggcagctg cagagacttt gagtgaagta gcctaagagg atttttaga 2450  
gaatccgtat tgaatttgtg tggtatgtca ctcagaaaga atcgtaatgg 2500  
gtatattgat aaattttaaa attggatatat ttgaaataaa gttgaatatt 2550  
atatataa 2558.

<210> 618  
<211> 750  
<212> PRT  
<213> Homo Sapien

<400> 618

Met	Trp	Asn	Leu	Leu	His	Glu	Thr	Asp	Ser	Ala	Val	Ala	Thr	Ala
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Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly
				20					25				30	
Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser
					35			40				45		
Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala
					50			55				60		
Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His
					65			70				75		
Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe
					80			85				90		
Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu
					95			100				105		
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro
					110			115				120		
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly
					125			130				135		
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly
					140			145				150		
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser
					155			160				165		
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala
					170			175				180		
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn
					185			190				195		
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg
					200			205				210		

Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val  
215 220 225

Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys  
230 235 240

Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg  
245 250 255

Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro  
260 265 270

Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu  
275 280 285

Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr  
290 295 300

Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro  
305 310 315

Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly  
320 325 330

Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His  
335 340 345

Ile His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly  
350 355 360

Thr Leu Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly  
365 370 375

Gly His Arg Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser  
380 385 390

Gly Ala Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu  
395 400 405

Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser  
410 415 420

Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala  
425 430 435

Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile  
440 445 450

Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp  
455 460 465

Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu  
470 475 480

Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu  
485 490 495

Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro  
500 505 510

Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe  
515 520 525

Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn  
530 535 540

Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val  
545 550 555

Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe  
560 565 570

Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Gly Met Val Phe  
575 580 585

Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Arg Asp Tyr  
590 595 600

Ala Val Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser  
605 610 615

Met Lys His Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp  
620 625 630

Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys  
635 640 645

Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro Ile Val  
650 655 660

Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg Ala Phe  
665 670 675

Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val  
680 685 690

Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe  
695 700 705

Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp  
710 715 720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala  
725 730 735

Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala  
740 745 750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619  
agatgtgaag gtgcaggtgt gccg 24

<210> 620  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620  
gaacatcagc gctcccgta attcc 25

<210> 621  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621  
ccagccttg aatggtacaa aggagagaag aagctttca atggcc 46

<210> 622  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622  
ccaaactcac ccagttagtg tgagc 25

<210> 623  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623  
tggaaatca ggaatggtgt tctcc 25

<210> 624  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe

<400> 624

cttgtttca ccattggct aacttgctg ctaggagttc aagccatgcc 50